



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 140902

TO: Karen A Lacourciere
Location: REM-2D15/2C18
Art Unit: 1635
Wednesday, December 29, 2004

Case Serial Number: 08945805

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518 *BOB*

barbara.obryen@uspto.gov

Search Notes

This Page Blank (uspto)

STIC-Biotech/ChemLib

140902

From: Lacourciere, Karen
Sent: Monday, December 20, 2004 3:00 PM
To: STIC-Biotech/ChemLib
Subject: RE: Sequence search request 90/006175

Please search this using the CRF from 08945805

Thank-you!

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Monday, December 20, 2004 2:52 PM
To: Lacourciere, Karen
Subject: RE: Sequence search request 90/006175

There is no valid CRF for this serial number, please provide us with another valid serial number. Thank you. Linda

-----Original Message-----

From: Lacourciere, Karen
Sent: Monday, December 20, 2004 2:33 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search request 90/006175

Please search SEQ ID NO:1 for 90/006,175 in both the commercial databases and in the pending files (interference)
Thank-you

Karen A. Lacourciere Ph.D.
Remsen 2D15 GAU 1635
(571) 272-0759

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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SEQUENCE LISTING WARNING:

The sequence serial number you submitted was not listed in the CRF file. The attached search may not contain the exact sequence(s) listed under your serial number. The sequence listing used was in the CRF for an earlier serial number. The file wrapper of your case indicated it as a CIP, Divisional, Parent, Grandparent, Grandchild(ren) or Continuation of the earlier serial number.

Please remember that it is the examiner's responsibility to ensure that a case is in compliance with the sequence rules before allowing it.

*CRF from 08-945805 (US 626203
used for this search)*

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 28, 2004, 07:31:07 ; Search time 1772 Seconds
(without alignments)
533.744 Million cell updates/sec

Title: US-08-945-805-1

Perfect score: 20
Sequence: 1 ccttgaaggattccctcc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_cm.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	20	100.0	20	6	BD272318 Method fo
2	20	100.0	20	6	AX937169 Sequence
3	20	100.0	20	6	BD166242 Sequence
4	20	100.0	20	6	BD173898 Pharmaceu
5	20	100.0	36	6	AR211932 Sequence
6	20	100.0	36	6	AR491437 Sequence
7	20	100.0	46	6	AR211931 Sequence
8	20	100.0	46	6	AR491436 Sequence
9	20	100.0	130	6	AX824437 Sequence
10	20	100.0	397	11	G73338 Sequence
11	20	100.0	411	11	G73796 SGV-R137 Ge
12	20	100.0	604	11	G73795 SGV-R136 Ge
13	20	100.0	992	10	MMVCAM1B1
14	20	100.0	1032	6	AR174653 Sequence
15	20	100.0	1032	6	BD140422 Endotheli
16	20	100.0	2321	10	MUSVCAM01
17	20	100.0	2355	9	S50587
18	20	100.0	2396	9	MMVCAMA
19	20	100.0	2458	10	MMU42327

20	20	100.0	2501	6	CQ778548	CQ778548	Sequence
21	20	100.0	3418	10	BC029823	BC029823	Mus muscu
22	20	100.0	3691	6	AX188354	AX188354	Sequence
23	20	100.0	5607	9	HUMVCAM1A	M73255	Human vascu
24	20	100.0	22868	9	AF536818	AF536818	Homo sapi
25	20	100.0	152858	9	AC093428	AC093428	Homo sapi
26	20	100.0	194252	10	AC108909	AC108909	Mus muscu
c 27	20	100.0	228371	2	AC122888	AC122888	Mus muscu
c 28	20	100.0	268180	2	AC113762	AC113762	Rattus no
c 29	20	100.0	287919	2	AC109094	AC109094	Rattus no
c 30	18.4	92.0	110000	1	AE017180_15	Continuation (16 o	
31	18	90.0	19	6	AR211934	AR211934	Sequence
32	18	90.0	19	6	AR491439	AR491439	Sequence
33	18	90.0	160765	2	AC136005	AC136005	Homo sapi
34	18	90.0	161027	9	AC136006	AC136006	Homo sapi
35	18	90.0	169073	8	AC132491	AC13491	Oryza sat
c 36	18	90.0	179599	2	AC112930	AC112930	Mus muscu
37	18	90.0	213073	9	AC092653	AC092653	Homo sapi
38	17.4	87.0	63	6	AX824455	AX824455	Sequence
c 39	17.4	87.0	63	6	AX824456	AX824456	Sequence
40	17.4	87.0	1360	14	AY486462	AY486462	Hyposter
c 41	17.4	87.0	90354	9	AP001124	AP001124	Homo sapi
42	17.4	87.0	166860	10	AC115924	AC115924	Mus muscu
c 43	17.4	87.0	179080	2	AC092514	AC092514	Papio anu
44	17.4	87.0	203822	2	AC146825	AC146825	Otolemur
45	17.4	87.0	219796	2	AC146734	AC146734	Otolemur

ALIGNMENTS

RESULT 1
BD272318

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BD272318 20 bp DNA linear PAT 17-JUL-2003
Method for determining whether a certain compound is able to
inhibit the interaction of peptide with receptor of advanced
glycation end product (RAGE).

BD272318 GI:33082086

JP 2002526758-A/1.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

Schmidt,A.M. and Stern,D.

Method for determining whether a certain compound is able to

inhibit the interaction of peptide with receptor of advanced

glycation end product (RAGE)

Patent: JP 2002526758-A 1 20-AUG-2002;

THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK

OS Homo sapiens (human)

PN JP 2002526758-A/1

PD 20-AUG-2002

PF 05-OCT-1999 JP 2000574569

PR 05-OCT-1998 US 09/166649

PI ANN MARIE SCHMIDT,DAVID STERN

PC GOIN33/50,A61K9/12,A61K9/127,A61K9/50,A61K31/472,A61K45/00, PC

A61P3/00,

PC

A61P3/04,A61P3/10,A61P3/12,A61P29/00,A61P37/06,C12Q1/02,C12Q1/ PC

68,

GOIN33/15//C12N5/10,C12N5/00

CC Primer Against Human NF-kB

CC PCR Primer Against Human NF-kB

CC Key Location/Qualifiers

FT source 1..20

FT Location/Qualifiers

1..20

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

Wed Dec 29 09:34:01 2004

us-08-945-805-1.rge

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  Best Local Similarity 100.0%; Pred. No. 7.6;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 1 CCTTGAAGGGATTTCCTCC 20
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  DB 1 CCTTGAAGGGATTTCCTCC 20

RESULT 2
AX937169 AX937169 20 bp DNA linear PAT 06-JAN-2004
LOCUS Sequence 9 from Patent WO03091432.
ACCESSION AX937169
VERSION AX937169.1 GI:40713277
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Lee, I.K. and Morishita, R.
TITLE Circular dumbbell decoy oligodeoxynucleotides (cdodn) containing
        dna bindings sites of transcription factors
JOURNAL Patent: WO 03091432-A 9 06-NOV-2003;
        Anges MG, Inc. (JP) ; Lee, In-Kyu (KR)
FEATURES
  source
    1..20
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Description of Artificial Sequence: NF-7B decoy"

ORIGIN
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  DB 1 CCTTGAAGGGATTTCCTCC 20

RESULT 3
BD166242 BD166242 20 bp DNA linear PAT 17-JAN-2003
LOCUS Pharmacetical composition containing decoy and utilization
DEFINITION thereof.
ACCESSION BD166242
VERSION BD166242.1 GI:27872054
KEYWORDS JP 2002193813-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS Morishita, R., Aoki, M., Ogiwara, T. and Kawasaki, T.
TITLE Pharmacetical composition containing decoy and utilization thereof
JOURNAL Patent: JP 2002193813-A 1 10-JUL-2002;
        MEDGENE BIOSCIENCE INC
COMMENT OS Artificial Sequence
        PN JP 2002193813-A/1
        PD 10-JUL-2002
        PF 27-DEC-2000 JP 2000399613
        PI RYUICHI MORISHITA, MOTOKUNI AOKI, TOSHIO OGIWARA, TOMIO KAWASAKI
        PC A61K31/00, A61K47/46, A61P9/00, A61P11/06, A61P13/12,
        PC A61P17/00,
        PC A61P29/00, A61P35/00, C12N15/09, C12N15/00
        CC Description of Artificial Sequence: NF-kappaB decoy FH Key
        Location/Qualifiers
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  DB 1 CCTTGAAGGGATTTCCTCC 20

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BD173898 BD173898 20 bp DNA linear PAT 18-FEB-2003
LOCUS Pharmaceutical compositions containing decoy and method of using
DEFINITION the same.
ACCESSION BD173898
VERSION BD173898.1 GI:28415231
KEYWORDS WO 02066070-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Morishita, R., Aoki, M., Ogiwara, T., Kaneda, Y. and Nakamura, H.
TITLE Pharmaceutical compositions containing decoy and method of using
        the same
JOURNAL Patent: WO 02066070-A 1 29-AUG-2002;
        ANGES MG INC, RYUICHI MORISHITA, MOTOKUNI AOKI, TOSHIO OGIWARA,
        YASUFUMI KANEDA, HIROSHIGE NAKAMURA
COMMENT OS Artificial Sequence
        PN WO 02066070-A/1
        PD 29-AUG-2002
        PF 06-FEB-2002 WO 2002JP000990
        PR 20-FEB-2001 JP 01P 044350
        PI RYUICHI MORISHITA, MOTOKUNI AOKI, TOSHIO OGIWARA, YASUFUMI
        KANEDA,
        PI HIROSHIGE NAKAMURA
        PC A61K48/00, A61K31/711, A61K9/06, A61K47/06, A61K47/10, A61P17/00,
        PC A61P17/04
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FEATURES
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      |||||
  DB 1 CCTTGAAGGGATTTCCTCC 20

RESULT 5
AR211932 AR211932 36 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 2 from patent US 6399376.
DEFINITION
ACCESSION AR211932
VERSION AR211932.1 GI:21515384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
          Unclassified.

```


REFERENCE 1 (bases 1 to 36)
AUTHORS Medford,R.M. and Bennett,C.Frank.
TITLE Modulation of vascular cell adhesive molecule expression through
oligonucleotide interactions
JOURNAL Patent: US 6399376-A 2 04-JUN-2002;
FEATURES Location/Qualifiers
source
1..36
/organism="unknown"
/mol_type="unassigned DNA"

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Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAAGGGATTCCCTCC 20
Db 16 CCTGAAGGGATTCCCTCC 35

RESULT 6
AR491437
LOCUS AR491437 36 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 2 from patent US 6713621.
ACCESSION AR491437
VERSION AR491437.1 GI:47259436
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 36)
AUTHORS Medford,R.M. and Bennett,C.F.
TITLE Chimeric oligonucleotides for modulating gene expression
JOURNAL Patent: US 6713621-A 2 30-MAR-2004;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="genomic DNA"

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Query Match 100.0%; Score 20; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAAGGGATTCCCTCC 20
Db 16 CCTGAAGGGATTCCCTCC 35

RESULT 7
AR211931
LOCUS AR211931 46 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 1 from patent US 6399376.
ACCESSION AR211931
VERSION AR211931.1 GI:21515383
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 46)
AUTHORS Medford,R.M. and Bennett,C.Frank.
TITLE Modulation of vascular cell adhesive molecule expression through
oligonucleotide interactions
JOURNAL Patent: US 6399376-A 1 04-JUN-2002;
FEATURES Location/Qualifiers
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/organism="unknown"
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Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 CCTGAAGGGATTCCCTCC 40

RESULT 8
AR491436
LOCUS AR491436 46 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 1 from patent US 6713621.
ACCESSION AR491436
VERSION AR491436.1 GI:47259435
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 46)
AUTHORS Medford,R.M. and Bennett,C.F.
TITLE Chimeric oligonucleotides for modulating gene expression
JOURNAL Patent: US 6713621-A 1 30-MAR-2004;
FEATURES Location/Qualifiers
source
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Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAAGGGATTCCCTCC 20
Db 21 CCTGAAGGGATTCCCTCC 40

RESULT 9
AX824437
LOCUS AX824437 130 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 16 from Patent WO03071281.
ACCESSION AX824437
VERSION AX824437.1 GI:39750436
KEYWORDS
SOURCE Synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boersma,C.J. and van Gool,A.J.
TITLE Estrogen receptor interaction with a transcription factor
JOURNAL Patent: WO 03071281-A 16 28-AUG-2003;
Akzo Nobel N.V. (NL)
FEATURES Location/Qualifiers
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="VCAM-1, Sequence of cloned part on page 32 lines
4-7"

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Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAAGGGATTCCCTCC 20
Db 34 CCTGAAGGGATTCCCTCC 53

RESULT 10
G73338
LOCUS G73338 397 bp DNA linear STS 28-DEC-2002
DEFINITION SGW-R233 Genomic DNA from human peripheral blood leukocytes Homo
sapiens STS genomic 5' and 3', sequence tagged site.

Wed Dec 29 09:34:01 2004

RESULT 11
 G73796
 LOCUS
 DEFINITION
 SGV-R137 Genomic DNA from human peripheral blood leukocytes Homo sapiens STS genomic 5' and 3', sequence tagged site.
 G73796
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 397)
 Taylor,J.G., Tang,D., Savage,S., Leitman,S.F., Heller,S.I., Serjeant,G.R., Rodgers,G.P. and Chanock,S.J.
 Variants in the VCAM1 gene and risk for symptomatic stroke in sickle cell disease
 Unpublished (2001)
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Contact: Stephen J. Chanock
 Section of Genomic Variation, Pediatric Oncology Branch, Center for Cancer Research, National Cancer Institute
 National Institutes of Health
 NCI Advanced Technology Center, 8717 Grovemont Circle,
 Gaithersburg, MD 20877, USA
 Email: sc83a@nih.gov
 Primer A: AGTGAAGGATTCCTGCTGGTG
 Primer B: TCACCTACTATCGCAAACTGACTG
 STS size: 397
 PCR Profile:
 Preincubation: 95 degrees C for 600 seconds
 Denaturation: 94 degrees C for 30 seconds
 Annealing: 63 degrees C for 30 seconds
 Extension: 72 degrees C for 40 seconds
 Final Extension: 72 degrees C for 600 seconds
 PCR Cycles: 40
 Thermal cycler: MJ Research model PTC-225
 Protocol:
 Template: 10-50 ng
 each 0.5 uM
 Primer: each 200 uM
 dNTPs: 0.025 units/ul
 AmpliTaqGold Polymerase: 20 ul
 Total Vol: 1X volume
 Buffer: 1.8 mM
 MgCl2
 Applied Biosystems 10X PCR Buffer II
 5' upstream region.
 Location/Qualifiers
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 1..397
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 complement(374..397)
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 |||||
 DB 59 CCTTGAAGGATTCCTCC 78
 |||||

RESULT 11
 G73796
 LOCUS
 DEFINITION
 SGV-R137 Genomic DNA from human peripheral blood leukocytes Homo sapiens STS genomic 5' and 3', sequence tagged site.
 G73796
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 411)
 Taylor,J.G., Tang,D., Savage,S., Leitman,S.F., Heller,S.I., Serjeant,G.R., Rodgers,G.P. and Chanock,S.J.
 Variants in the VCAM1 gene and risk for symptomatic stroke in sickle cell disease
 Unpublished (2001)
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Contact: Stephen J. Chanock
 Section of Genomic Variation, Pediatric Oncology Branch, Center for Cancer Research, National Cancer Institute
 National Institutes of Health
 NCI Advanced Technology Center, 8717 Grovemont Circle,
 Gaithersburg, MD 20877, USA
 Email: sc83a@nih.gov
 Primer A: TTTTTCCTCCTCCACCC
 Primer B: AACCTTATTTGTGCCACCTG
 STS size: 411
 PCR Profile:
 Preincubation: 95 degrees C for 600 seconds
 Denaturation: 94 degrees C for 30 seconds
 Annealing: 63 degrees C for 30 seconds
 Extension: 72 degrees C for 40 seconds
 Final Extension: 72 degrees C for 600 seconds
 PCR Cycles: 40
 Thermal cycler: MJ Research model PTC-225
 Protocol:
 Template: 10-50 ng
 each 0.5 uM
 Primer: each 200 uM
 dNTPs: 0.025 units/ul
 AmpliTaqGold Polymerase: 20 ul
 Total Vol: 1X volume
 Buffer: 1.8 mM
 MgCl2
 Applied Biosystems 10X PCR Buffer II
 5' upstream region.
 Location/Qualifiers
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 primer_bind
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 complement(389..411)
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 Best Local Similarity 100.0%; Pred. No. 6.9; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20
 Db 262 CCTTGAAGGGATTTCCTCC 281

RESULT 12

G73795 604 bp DNA linear STS 28-DEC-2002
 LOCUS SGV-R136 Genomic DNA from human peripheral blood leukocytes Homo
 DEFINITION sapiens STS genomic 5' and 3', sequence tagged site.

ACCESSION G73795

VERSION G73795.1 GI:27413075

KEYWORDS STS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 604)

Serjeant,G.R., Rodgers,G.P. and Chanock,S.J.

Taylor,J.G., Tang,D., Savage,S., Leitman,S.F., Heller,S.I.,

variants in the VCAM1 gene and risk for symptomatic stroke in

sickle cell disease

Unpublished (2001)

JOURNAL

COMMENT

Contact: Stephen J. Chanock

Section of Genomic Variation, Pediatric Oncology Branch, Center for

Cancer Research, National Cancer Institute

National Institutes of Health

NCI Advanced Technology Center, 8717 Grovemont Circle,

Gaithersburg, MD 20877, USA

Email: sc83@nih.gov

Primer A: GAAGTTATGTCGTCCTTTT

Primer B: AACCTTATTGTGTCAC

STS size: 604

PCR Profile:

Preincubation: 95 degrees C for 600 seconds

Denaturation: 94 degrees C for 30 seconds

Annealing: 55 degrees C for 30 seconds

Extension: 72 degrees C for 40 seconds

Final Extension: 72 degrees C for 600 seconds

PCR Cycles: 40

Thermal cycler: MJ Research model PTC-225

Protocol:

Template: 10-50 ng

Primer: each 0.5 uM

dNTPs: each 200 uM

AmpliTaqGold Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2 1.8 mM

Applied Biosystems 10X PCR Buffer II 1X volume

5' upstream region.

Location/Qualifiers

1. .604

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone_lib="Genomic DNA from human peripheral blood

leukocytes"

/note="Human genomic DNA prepared from either fresh or

immortalized peripheral blood leukocytes"

1. .604

/gene="VCAM1"

/note="vascular cell adhesion molecule 1"

1. .604

/gene="VCAM1"

1. .22

/gene="VCAM1"

complement (585. .604)

Query Match 100.0%; Score 20; DB 11; Length 604;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20

Db 455 CCTTGAAGGGATTTCCTCC 474

RESULT 13

MMVCAM1B1 992 bp DNA linear ROD 03-MAY-2000
 LOCUS Mus musculus NIH Swiss vascular cell adhesion molecule-1 (VCAM-1)
 DEFINITION gene, exon 1, partial cds.

ACCESSION U12878

VERSION U12878.1 GI:1041794

KEYWORDS 1 of 6

SEGMENT Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 796; 808 to 824)

Kumar,A.G., Dai,Y.X., Kozak,C.A., Mims,M.P., Gotto,A.M. and

Ballantyne,C.M.

Murine VCAM-1: Molecular cloning, Mapping, and Analysis of a

Truncated Form

Unpublished

REFERENCE 2 (bases 1 to 992)

Kumar,A.G.

Direct Submission

Submitted (02-AUG-1994) Ajith G. Kumar, Department of Medicine,

Baylor College of Medicine, 6535 Fannin Street, Houston, TX 77030,

USA

COMMENT On Oct 28, 1995 this sequence version replaced gi:531856.

FEATURES

Location/Qualifiers

1. .992

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="NIH Swiss"

/db_xref="taxon:10090"

/chromosome="3"

/clone="lambda 1"

/cell_line="NIH3T3"

/cell_type="fibroblast"

/clone_lib="Genomic library lambda FIX II, Stratagene, La

Jolla, CA"

/dev_stage="adult"

TATA_signal 632. .636

CDS 751. .814

/gene="VCAM-1"

/codon_start=1

/product="vascular cell adhesion molecule-1"

/protein_id="AAB60659.1"

/db_xref="GI:531863"

/translation="MPVKMVAVLGASTVLWILFAV"

751. .814

/gene="VCAM-1"

<751. .814

/gene="VCAM-1"

/number=1

sig_peptide

exon

ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 992;

Best Local Similarity 100.0%; Pred. No. 6.7;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20

Db 592 CCTTGAAGGGATTTCCTCC 611

RESULT 14

Wed Dec 29 09:34:01 2004

AR174653 LOCUS 1032 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 8 from patent US 6307025.
ACCESSION AR174653
VERSION AR174653.1 GI:17914973
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1032)
AUTHORS Hession,C.A., Lobb,R.R., Goelz,S.E., Osborn,L., Benjamin,C.D. and Rosa,M.D.
TITLE VCAM fusion proteins and DNA coding therefor
JOURNAL Patent: US 6307025-A 8 23-OCT-2001;
FEATURES Location/Qualifiers
source 1..1032
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1032;
Best Local Similarity 100.0%; Pred. No. 6.7; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTGAAGGGATTCCCTCC 20
|||||
Db 221 CCTTGAAGGGATTCCCTCC 240

RESULT 15

BD140422 1032 bp DNA linear PAT 18-SEP-2002
LOCUS Endothelial-leukocyte adhesion molecule (ELAM) and molecule
DEFINITION participating in leukocyte adhesion (MILA).
ACCESSION BD140422
VERSION BD140422.1 GI:23235367
KEYWORDS JP 2002065285-A/6
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1032)
AUTHORS Hession,C.R., Lobb,R.R., Goelz,S.E., Osborne,L., Benjamin,C.D. and Rosa,M.D.
TITLE Endothelial-leukocyte adhesion molecule (ELAM) and molecule
JOURNAL Participating in leukocyte adhesion (MILA)
Patent: JP 2002065285-A 6 05-MAR-2002;
BIOGEN INC

COMMENT

OS Homo sapiens (human)
PN JP 2002065285-A/6
PD 05-MAR-2002
PF 18-JUN-2001 JP 2001184133 359516 PR
PR 28-APR-1989 US 345151,01-JUN-1989 US
18-DEC-1989 US 452675
PI CATHERINE R HESSON,ROY R LOBB,SUSAN E GOELZ,LAURELY OSBORNE,
PI CHRISTOPHER D BENJAMIN,MARGARET D ROSA
PC C12N15/09,A61K35/16,A61K38/00,A61K45/00,A61K48/00,A61P1/00, PC
A61P17/00,
PC A61P35/00,C07K14/47,C07K16/18,C07K16/42,C12N1/15,C12N1/19, PC
C12N1/21,
PC
C12N5/10,C12N5/10,C12N5/10,C12N15/02,C12P21/02,C12P21/08,C12Q1/ PC
02,
G01N33/15,G01N33/50,G01N33/53,G01N33/53,G01N33/566,G01N33/577,
PC C12N15/00,
PC C12N15/00,C12N15/00,A61K37/02,C12N5/00 CC
PC C12N5/00,C12N15/00,A61K37/02,C12N5/00 CC
Endothelial-leukocyte adhesion molecule (ELAM) and molecule CC
participating
CC in leukocyte adhesion (MILA)
FH Key Location/Qualifiers
FT source 1..1032
FT /organism="Homo sapiens (human)".
FT Location/Qualifiers

FEATURES

source 1..1032
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1032;
Best Local Similarity 100.0%; Pred. No. 6.7; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTGAAGGGATTCCCTCC 20
|||||
Db 221 CCTTGAAGGGATTCCCTCC 240
Search completed: December 28, 2004, 10:45:37
Job time : 1778 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2004, 07:31:07 ; Search time 399 Seconds
(without alignments)
263.129 Million cell updates/sec

Title: US-08-945-805-1

Perfect score: 20

Sequence: 1 cctgaaggattccctcc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2	AAT69675
2	20	100.0	20	3	AA14365
3	20	100.0	20	4	AAH43069
4	20	100.0	20	6	ABV72301
5	20	100.0	20	6	AB54472
6	20	100.0	20	9	ACC79778
7	20	100.0	20	10	ADD69731
8	20	100.0	20	10	ADP53868
9	20	100.0	20	10	ADG43792
10	20	100.0	20	12	ADM96331
11	20	100.0	20	12	ADM91765
12	20	100.0	20	12	ADP83986
13	20	100.0	36	2	AAQ90101
14	20	100.0	47	2	AAQ90100
15	20	100.0	130	10	ACF79417
16	20	100.0	1024	10	ABZ83493
17	20	100.0	1032	2	AAQ06690
18	20	100.0	1032	6	AA17081
19	20	100.0	1032	10	ADH73058
20	20	100.0	2396	3	AA34966
21	20	100.0	2396	3	AAF21088

ALIGNMENTS

RESULT 1

AAT69675

ID AAT69675 standard; DNA; 20 BP.

XX AC AAT69675;

DT 04-AUG-1997 (first entry)

DE Transcription factor NF-kappa-B DNA binding site antagonist.
KW Decoy; antagonist; NF-kappa-B; NF-kB; transcription; regulation;
prevention; treatment; disease; ischaemia; inflammation;
autoimmune; cancer; metastasis; cachexia; organ; transplantation;
surgery; ds.

XX OS Synthetic.

XX PN WO9635430-A1.

XX PD 14-NOV-1996.

XX PF 10-MAY-1996; 96WO-JP001234.

XX PR 12-MAY-1995; 95JP-00114990.

XX PR 02-NOV-1995; 95JP-00285504.

XX PA (FUJI) FUJISAWA PHARM CO LTD.

XX PI Morishita R, Ogiwara T, Sugimoto T, Maeda K, Kawamura I, Chiba T;

XX DR WPI; 1996-518400/51.

XX PT Anti:sense NF-kB agent - for treatment of ischaemia, inflammatory disease

XX PS auto:immune disease, etc.

XX PS Claim 7; Page 9; 18pp; Japanese.

XX CC The present sequence is a decoy, which specifically antagonises the
nucleic acid site to which a NF-kappa-B transcription regulator binds. It
can be used to prevent or treat diseases caused by NF-kappa-B, e.g.
ischaemia, inflammatory and autoimmune disease, cancer metastasis and
cachexia, especially following organ transplant or surgery

XX SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

22 20 100.0 2396 10 ABZ96782 Abz96782 Human nuc
23 20 100.0 2396 11 ABD20631 Abd20631 Human pul
24 20 100.0 3689 4 AAH72882 Aah72882 Human cer
25 20 100.0 3691 4 AAH72772 Aah72772 Human cer
26 20 100.0 4616 3 AAA34968 Aaa34968 Human ade
27 20 100.0 4616 3 AAF21090 Aaf21090 Human low
28 20 100.0 4616 11 ABZ96784 Abz96784 Human nuc.
29 20 100.0 4616 10 ABD20633 Abd20633 Human pul
30 18 90.0 19 2 AAQ90103 Aaq90103 VCAM-1 ex
31 17.4 87.0 63 10 ACF79431 Acf79431 VCAM 3 PC
32 17.4 87.0 63 10 ACF79432 Acf79432 VCAM 3 PC
33 17 85.0 708 6 ABZ42918 Abz42918 Human gpc
34 16.8 84.0 37 11 ADL76518 Adl76518 Human ptg
35 16.8 84.0 40 12 ADG13972 Adg13972 Human egf
36 16.8 84.0 40 12 ADG13997 Adg13997 Human egf
37 16.8 84.0 40 12 ADG14001 Adg14001 Human egf
38 16.8 84.0 40 12 ADG14005 Adg14005 Human egf
39 16.8 84.0 40 12 ADG13983 Adg13983 Human egf
40 16.8 84.0 40 12 ADG14002 Adg14002 Human egf
41 16.8 84.0 40 12 ADG13980 Adg13980 Human egf
42 16.8 84.0 40 12 ADG13979 Adg13979 Human egf
43 16.8 84.0 40 12 ADG13981 Adg13981 Human egf
44 16.8 84.0 40 12 ADG13989 Adg13989 Human egf
45 16.8 84.0 40 12 ADG13976 Adg13976 Human egf

```

CC with an AGE
XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
Db 1 CCTTGAAGGGATTTCCTCC 20

RESULT 2
AA14365
ID AAA14365 standard; DNA; 20 BP.
XX
AC AAA14365;
XX
DT 15-AUG-2000 (first entry)
XX
DE Human NF-kappa-B binding site EMSA probe.
XX
KW NK-kappa-B binding site; nuclear factor-kappa-B; EMSA;
KW electrophoretic mobility shift assay; advanced glycation end-product;
KW AGE; receptor for AGE; RAGE; interaction inhibitor; kidney failure;
KW diabetes; systemic lupus erythematosus; inflammatory lupus nephritis;
KW obesity; amyloidosis; inflammation; ageing; ds.
XX
OS Homo sapiens.
XX
PN WO200020458-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US022245.
XX
PR 05-OCT-1998; 98US-00166649.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Schmidt AM, Stern D;
XX
DR WPI; 2000-303750/26.
XX
PT Determining inhibitors of interaction between an advanced glycation
PT endproduct and its receptor, useful to develop therapeutics for various
PT associated conditions including diabetes and inflammatory lupus
PT nephritis.
XX
PS Example 1; Page 30; 66pp; English.
XX
CC The invention relates to a novel method for determining whether a
CC compound can inhibit interaction of an advanced glycation end-product
CC (AGE) or fragment thereof with the receptor for AGEs (RAGE). The method
CC comprises admixing the AGE (which has its amino groups inactivated by
CC chemical derivatization), RAGE, and the compound; determining the amount
CC of peptide bound to RAGE, and comparing this amount to the amount of
CC binding in the absence of the compound. A decrease in AGE/RAGE binding in
CC the presence of the compound indicates that the compound is an inhibitor.
CC Exemplary inhibitory compounds identified via the method are quinine,
CC quinidine, or derivatives with the same overall charge as these
CC compounds. AGEs are a class of compounds with heterogeneous structures
CC that result from the process of glycooxidation. The accumulation of AGEs
CC has been linked to a range of complications that occur in disorders such
CC as ageing, diabetes, renal failure and inflammation. Interaction of an
CC AGE with RAGE triggers multiple mechanisms, including the activation of
CC NF-kappa-B (nuclear factor kappa-B) which result in cellular perturbation
CC and dysfunction. Compounds which inhibit the interaction between AGEs and
CC RAGE may be used to treat kidney failure, diabetes, systemic lupus
CC erythematosus, inflammatory lupus nephritis, obesity, amyloidosis or
CC inflammation. Administration of such compounds may also be of benefit to
CC elderly individuals, particularly humans, other primates, mice, rats or
CC dogs. The present sequence represents an NF-kappa-B binding site probe
CC used in electrophoretic mobility shift assays (EMSA) of nuclear extracts
CC of human umbilical vein endothelial cells (HUEVCs) previously treated

```

ABV72301
 ID ABV72301 standard; DNA; 20 BP.
 XX
 AC ABV72301;
 XX
 DT 16-DEC-2002 (first entry)
 XX
 DE Nucleotide sequence of nuclear factor (NF)-kappaB decoy.
 XX
 KW Nuclear factor-kappaB; NF-kappa B; decoy; ets; disease; ds.
 XX
 OS Synthetic.
 XX
 PN JP2002193813-A.
 XX
 PD 10-JUL-2002.
 XX
 PF 27-DEC-2000; 2000JP-00399613.
 XX
 PR 27-DEC-2000; 2000JP-00399613.
 XX
 PA (ANJE-) ANJESU MG KK.
 XX
 DR WPI; 2002-660723/71.
 XX
 XX A pharmacological composition containing a decoy compound for treating
 PT diseases caused by the expression of a gene controlled by NF-kappaB or
 PT ets.
 XX
 PS Example 1; Page 9; 18pp; Japanese.
 XX
 CC The present sequence represents a synthetic nuclear factor (NF)-kappa B
 CC decoy. The specification describes a pharmacological composition for
 CC treating and preventing diseases caused by the expression of a gene
 CC controlled by NF-kappaB or ets. The composition comprises at least one
 CC decoy compound and a pharmacologically allowable carrier. The composition
 CC is used for treating diseases caused by the expression of a gene
 CC controlled by NF-kappaB or ets
 XX
 SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
 XX
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 1 CCTTGAAGGGATTTCCTCC 20
 Db 1 CCTTGAAGGGATTTCCTCC 20
 XX
 RESULT 5
 ABS54472
 ID ABS54472 standard; DNA; 20 BP.
 XX
 AC ABS54472;
 XX
 DT 11-DEC-2002 (first entry)
 XX
 DE Nuclear factor (NF)-kappa B decoy oligonucleotide.
 XX
 KW NF-kappa B; ss; drug composition; skin disease; decoy;
 KW nuclear factor-kappa B; signal transducer and activator of transcription;
 KW STAT-1; STAT-6; GATA-3; activator protein-1; AP-1; Ets;
 KW atopic dermatitis; psoriasis vulgaris; contact dermatitis; keloid;
 KW bedsores; ulcerative colitis; Crohn's disease.
 XX
 OS Synthetic.
 XX
 PN WO200266070-A1.
 XX
 PD 29-AUG-2002.
 XX
 PF 06-FEB-2002; 2002WO-JP000990.
 XX
 20-FEB-2001; 2001JP-00044350.
 (ANGE-) ANGES MG INC.
 Morishita R, Aoki M, Ogiwara T, Kaneda Y, Nakamura H;
 WPI; 2002-732717/79.
 Compositions for treating diseases, such as, atopic dermatitis, psoriasis
 vulgaris, contact dermatitis, and ulcerative colitis comprises decoys of
 e.g. nuclear factor-kappaB, and signal transducer and activator of
 transcription.
 Disclosure; Page 8; 41pp; Japanese.
 The invention discloses drug compositions for treating skin diseases
 containing a decoy and a pharmaceutically-acceptable carrier. The decoy
 oligonucleotides affect genes including nuclear factor (NF)-kappa B,
 signal transducer and activator of transcription (STAT)-1 and 6, GATA-3,
 activator protein (AP)-1 and Ets. The drug compositions are applicable in
 treating skin diseases like atopic dermatitis, psoriasis vulgaris,
 contact dermatitis, keloid, bedsores, ulcerative colitis or Crohn's
 disease. The sequence presented is the decoy oligonucleotide for NF-kappa
 B
 Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCTTGAAGGGATTTCCTCC 20
 Db 1 CCTTGAAGGGATTTCCTCC 20
 RESULT 6
 ACC79778
 ID ACC79778 standard; DNA; 20 BP.
 XX
 AC ACC79778;
 XX
 DT 29-AUG-2003 (first entry)
 XX
 DE Nuclear factor-kappa B (NF-kappa-B) decoy oligonucleotide SEQ ID NO:1.
 XX
 KW Pharmaceutical composition; organ transplantation rejection inhibition;
 KW immunosuppressive; regeneration; transplantation medicine;
 KW kidney transplant; nuclear factor-kappa B; NF-kappa-B; ss.
 XX
 OS Synthetic.
 XX
 PN WO2003043663-A1.
 XX
 PD 30-MAY-2003.
 XX
 PF 20-NOV-2002; 2002WO-JP012142.
 XX
 PR 22-NOV-2001; 2001JP-00358587.
 XX
 PA (ANGE-) ANGES MG INC.
 XX
 PI Morishita R, Tomita N, Ogiwara T, Higashi N;
 WPI; 2003-541462/51.
 Pharmaceutical compositions, useful for the suppression of rejection in
 organ transplantation e.g. kidney transplants, comprises a nuclear
 transcription factor (NF-kappa-B) decoy compound and optionally an
 ultrasonic test contrast medium.
 Example; Page 10; 42pp; Japanese.

CC and may be useful for the prevention of brain and nerve injury following
 CC disorders associated with cerebral ischaemia, such as sub-cranial
 CC membrane bleeding, hypertensive intracranial bleeding, cerebral
 CC infarction, brain tumour or chronic or acute subdural haematoma. The
 CC current sequence is that of the cerebral ischaemia-related NF-kappaB
 CC decoy DNA of the invention.
 XX
 SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;
 QY 1 CCTTGAAGGGATTCCCTCC 20
 DB 1 CCTTGAAGGGATTCCCTCC 20
 RESULT 8
 ADF53868
 ID ADF53868 standard; DNA; 20 BP.
 XX
 AC ADF53868;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Circular dumbbell oligodeoxynucleotide related oligo, SEQ ID No 9.
 KW circular dumbbell oligodeoxynucleotide; CDODN; DNA-binding domain;
 KW transcriptional factor; vasotropic; antiinflammatory; gastrointestinal;
 KW dermatological; antiarteriosclerotic; antiatherosclerotic; cytostatic;
 KW antiasthmatic; gene therapy; AP-1 decoy; E2F decoy;
 KW vascular smooth muscle cell proliferation; neointimal hyperplasia;
 KW restenosis; prophylaxis; exonuclease; ss.
 XX
 OS Unidentified.
 XX
 FN WO2003091432-A1.
 XX
 PD 06-NOV-2003.
 XX
 PF 26-APR-2002; 2002WO-JP004303.
 XX
 PR 26-APR-2002; 2002WO-JP004303.
 XX
 PA (ANGE-) ANGES MG INC.
 PA (LEBI/) LEE I.
 XX
 PI Lee I, Morishita R;
 XX
 DR WPI; 2003-877331/81.
 XX
 PT New circular dumbbell oligonucleotide comprising two loops and a stem
 PT structure capable of binding the DNA-binding domain of AP-1, E2F or
 PT NFkappaB, useful in treating or preventing vascular smooth muscle cell
 PT proliferation.
 XX
 PS Disclosure; SEQ ID NO 9; 142pp; English.
 XX
 CC The invention relates to a novel circular dumbbell oligodeoxynucleotide
 CC (CDODN) comprising two loop structures and a stem structure, where the
 CC stem structure comprises a nucleotide sequence capable of binding the DNA
 CC -binding domain of a transcriptional factor. The invention further
 CC comprises a method for treating or preventing a disease or disorder
 CC related to a transcriptional factor in a subject; and a pharmaceutical
 CC composition for treating or preventing a disease or disorder related to a
 CC transcriptional factor in a subject comprising a therapeutic amount of a
 CC CDODN described above and a pharmaceutical carrier. The CDODN oligo has
 CC the following activities: vasotropic, antiinflammatory, gastrointestinal,
 CC dermatological, antiarteriosclerotic, antiatherosclerotic, cytostatic, and
 CC antiasthmatic. The CDODN can be used in gene therapy. The CDODN are
 CC useful in the manufacture of a medicament for treating or preventing a
 CC disease or disorder related to a transcriptional factor in a subject. The

XX The present invention describes pharmaceutical compositions (A) for
 CC inhibiting rejection in organ transplantation which contain a nuclear
 CC factor-kappa B (NF-kappa-B) decoy compound. Also described: (1) a method
 CC for inhibiting rejection in organ transplantation by administering any of
 CC the remedies (A) to a donor organ before ultrasonication of the decoy
 CC compound-containing donor organ; (2) a method for improving prognosis of
 CC organ transplantation by administering any of the remedies (A) to a donor
 CC organ before ultrasonication of the decoy compound-containing donor organ
 CC ; and (3) a method for elevating transfection of an oligonucleotide into
 CC a biological tissue by administering such oligonucleotide to a donor
 CC organ before ultrasonication of the oligonucleotide-containing biological
 CC tissue. (A) have immunosuppressive activity, and can be used in NF-kappa-
 CC B inhibitors. The remedies (A) can be used in regeneration and
 CC transplantation medicine. Specifically, they are for inhibiting rejection
 CC in organ transplantation and improving its prognosis, particularly kidney
 CC transplants. The present sequence represents an NF-kappa-B decoy
 CC oligonucleotide, which is used in an example from the present invention
 XX
 SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;
 QY 1 CCTTGAAGGGATTCCCTCC 20
 DB 1 CCTTGAAGGGATTCCCTCC 20
 RESULT 7
 ADD69731
 ID ADD69731 standard; DNA; 20 BP.
 XX
 AC ADD69731;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Cerebral ischaemia-related NF-kappaB decoy DNA.
 KW cerebral ischaemia; nuclear factor kappaB; NF-kB decoy; neuroprotective;
 KW neurotropic; cerebroprotective; brain tumour; nerve injury;
 KW sub-cranial membrane bleeding; hypertensive intracranial; infarction;
 KW chronic; acute subdural haematoma; ds.
 XX
 OS Unidentified.
 XX
 FN WO2003082331-A1.
 XX
 PD 09-OCT-2003.
 XX
 PF 29-MAR-2002; 2002WO-JP003239.
 XX
 PR 29-MAR-2002; 2002WO-JP003239.
 XX
 PA (ANGE-) ANGES MG INC.
 PA (SAWA/) SAWA Y.
 XX
 PI Sawa Y, Morishita R, Kaneda Y, Matsuda H, Yoshimine T;
 XX
 DR WPI; 2003-812508/76.
 XX
 PT Transfection of NF-kB decoy oligonucleotide into brain tissue by carotid
 PT injection using a suitable carrier for treatment and prevention of
 PT disorders associated with cerebral ischemia.
 XX
 PS Example 1; SEQ ID NO 1; 79pp; Japanese.
 XX
 CC The invention relates to a novel drug composition for prevention and
 CC treatment of disorders associated with cerebral ischaemia which contains
 CC a nuclear factor kappaB (NF-kB) decoy oligonucleotide together with a
 CC suitable carrier for its transfection. The composition of the invention
 CC demonstrates neuroprotective, neurotropic and cerebroprotective activities

CC CDOON or the composition or the AP-1 decoy or E2F decoy is useful in
 CC treating or preventing a disease or disorder related to a transcriptional
 CC factor, e.g. vascular smooth muscle cell proliferation, neointimal
 CC hyperplasia following vessel injury or inflammatory bowel disease or in
 CC preventing restenosis and used in prophylaxis. Further diseases/disorders
 CC include inflammatory disease, dermatitis, aneurism, arteriosclerosis,
 CC atherosclerosis, angitis, cancer or asthma. The AP-1 decoy
 CC oligonucleotide with a CDOON is useful to avoid destruction by
 CC exonucleases. This sequence represents a circular dumbbell
 CC oligodeoxynucleotide related oligo of the invention.
 XX
 SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20
 Db 1 CCTTGAAGGGATTTCCTCC 20

RESULT 9

ADG43792
 ID ADG43792 standard; DNA; 20 BP.

XX AC ADG43792;

XX DT 26-FEB-2004 (first entry)

XX DE Synthetic NF-kappaB decoy SEQ ID NO:1.

XX KW NF-kappaB; cerebroprotective; cytostatic; ophthalmological; osteopathic;
 KW antiarthritic; antiasthmatic; dermatological; nephrotropic; periodontal;
 KW cerebral aneurysm; cancer; Marfan's syndrome; aortic dissection;
 KW postangioplastic reconstruction; rheumatoid arthritis; asthma;
 KW atopic dermatitis; renal insufficiency; plaque rupture; ss; etc.

XX OS Synthetic.

XX PN WO2003063911-A1.

XX PD 07-AUG-2003.

XX PF 01-FEB-2002; 2002WO-JP000865.

XX PR 01-FEB-2002; 2002WO-JP000865.

XX PA (ANGE-) ANGES MG INC.

XX PI Morishita R, Aoki M, Ogiwara T, Kawasaki T;

XX DR WPI; 2003-748040/70.

XX PT Composition for treating and preventing diseases caused by the expression
 of gene under regulation of NF-kappaB or ets comprises decoy and carrier.

XX PS Example 2; Page 19; 46pp; Japanese.

XX CC The invention relates to a novel composition for treating and preventing
 CC diseases caused by the expression of a gene under the regulation of NF-
 CC kappaB or ets comprises at least one decoy and a carrier. A composition
 CC of the invention has cerebroprotective, cytostatic, ophthalmological,
 CC osteopathic, antiarthritic, antiasthmatic, dermatological, nephrotropic,
 CC and periodontal activity. The composition is useful for treating and
 CC preventing diseases caused by the expression of a gene under the
 CC regulation of NF-kappaB or ets such as cerebral aneurysm, cancer, Marfan's
 CC syndrome, aortic dissection, postangioplastic reconstruction, rheumatoid
 CC arthritis, asthma, atopic dermatitis, renal insufficiency and plaque
 CC rupture. The present sequence represents an NF-kappaB decoy of the
 CC invention.

XX SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20
 Db 1 CCTTGAAGGGATTTCCTCC 20

RESULT 10

ADF69631
 ID ADF69631 standard; DNA; 20 BP.

XX AC ADF69631;

XX DT 26-FEB-2004 (first entry)

XX DE NF-kappaB binding site as decoy for inflammatory disease.

XX KW ss; antiinflammatory; antiarthritic; antirheumatic; antiarteriosclerotic;
 KW nephrotropic; inflammatory disease; joint disease;
 KW NF-Kappa B binding site; nephritis; hepatitis; renal failure;
 KW arteriosclerosis; glomerulonephritis; pyelonephritis; cystitis;
 KW prostatitis; urethritis; epididymitis; testitis; arthritis deformans;
 KW rheumatoid arthritis; peri-arthritis of shoulder;
 KW neck-shoulder-wrist syndrome.

XX OS Homo sapiens.

XX PN WO2003099339-A1.

XX PD 04-DEC-2003.

XX PF 20-MAY-2003; 2003WO-JP006299.

XX PR 29-MAY-2002; 2002JP-00156524.

XX PA (ANGE-) ANGES MG INC.

XX PI Tomita T, Yoshikawa H, Morishita R;

XX DR WPI; 2004-023234/02.

XX PT Remedies or preventing for inflammatory or joint diseases and disorders,
 e.g. rheumatoid arthritis, arthritis deformans and nephritis, containing
 decoy of NF-Kappa B or analogous transcriptional factor.

XX PS Disclosure; SEQ ID NO 1; 82pp; Japanese.

XX CC The invention relates to a drug composition for treating or preventing
 CC inflammatory or joint disease or disorders comprising at least 1 decoy of
 CC NF-Kappa B binding site. The NF-Kappa B decoy is preferably the
 CC nucleotide sequence GGATTTCC. The drugs are for inflammatory diseases
 CC and disorders, including nephritis, hepatitis, arthritis, acute/chronic
 CC renal failure, arteriosclerosis, glomerulonephritis, pyelonephritis,
 CC cystitis, prostatitis, urethritis, epididymitis and testitis,
 CC particularly arthritis deformans or rheumatoid arthritis, especially
 CC rheumatoid arthritis, as well as peri-arthritis of shoulder, neck-shoulder
 CC -wrist syndromes and secondary arthritis. This sequence corresponds to
 CC the NF-kappaB decoy.

XX SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20
 Db 1 CCTTGAAGGGATTTCCTCC 20

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us-08-945-805-1.1.rng

```

RESULT 11
ADP81765
ID ADM91765 standard; DNA; 20 BP.
XX
XX AC ADM91765;
XX
XX DT 17-JUN-2004 (first entry)
XX
XX DE Cis element decoy oligonucleotide #2.
XX
XX KW transplanted blood vessel; transcription factor; NF Kappa-B; cis element;
KW oligonucleotide; ss.
XX
XX OS Synthetic.
XX
XX PN WO2004026342-A1.
XX
XX PD 01-APR-2004.
XX
XX PF 27-DEC-2002; 2002WO-JP013805.
XX
XX PR 20-SEP-2002; 2002JP-00275884.
XX
XX PA (ANGE-) ANGES MG INC.
XX
XX PI Sawa Y, Shintani T, Matsuda H;
XX
XX DR WPI; 2004-295314/27.
XX
XX KW Method for controlling transcription transplanted blood vessels induced
PT by NF Kappa-B for preventing thickening.
XX
XX PS Disclosure; SEQ ID NO 2; 31pp; Japanese.
XX
XX CC The present invention relates to the method for controlling transcription
CC of blood vessels or transplanted blood vessels activated by transcription
CC factor NF kappa-B by placing them in contact with a decoy against NF
CC kappa-B. The method is used for preventing thickening in transplanted
CC blood vessels. The present sequence represents a cis element decoy
CC oligonucleotide.
XX
XX SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 12; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.9;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CCTTGAAGGGATTTCCTCC 20
XX DB 1 CCTTGAAGGGATTTCCTCC 20
XX
RESULT 12
ADP83986
ID ADP83986 standard; DNA; 20 BP.
XX
XX AC ADP83986;
XX
XX DT 26-AUG-2004 (first entry)
XX
XX DE Nuclear factor-kappaB decoy oligonucleotide #1.
XX
XX KW Nuclear factor-kappaB; NF-kappaB; ets; cerebral aneurysm; cancer;
KW Marfan's syndrome; aortic detachment; post-angioplasty restenosis;
KW chronic articular rheumatism; asthma; atopic dermatitis; nephritis;
KW renal failure; plaque rupture; eosinophilic abnormality; asthma;
KW bronchial asthma; childhood asthma; allergic asthma; atopic asthma;
KW steroid-resistant asthma; SRA; non-allergic asthma; intrinsic asthma;
KW extrinsic asthma; aspirin-induced asthma; cardiac asthma;
KW infectious asthma; allergy; skin disease; mycosis; vaccine; therapy; ss.
XX
XX OS Unidentified.
XX
XX PD

```

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PN US2004109843-A1.
XX
XX PD 10-JUN-2004.
XX
XX PF 10-JUL-2003; 2003US-00618362.
XX
XX PR 01-FEB-2002; 2002WO-JP000865.
XX
XX PA (MORI/) MORISHITA R.
XX (AOKI/) AOKI M.
XX (OGIH/) OGIHARA T.
XX (KAWA/) KAWASAKI T.
XX (MAKI/) MAKINO H.
XX
XX PI Morishita R, Aoki M, Ogiwara T, Kawasaki T, Makino H;
XX
XX DR WPI; 2004-448815/42.
XX
XX KW New compositions comprising at least one decoy, useful for the treating
XX and/or preventing a disease, disorder and/or condition caused by
XX expression of a gene controlled by NF-KB or ets, or by eosinophilic
XX abnormality, e.g. cancer.
XX
XX PS Example 1; SEQ ID NO 1; 37pp; English.
XX
XX CC The present invention provides a pharmaceutical composition for the
XX treatment and/or prevention of a disease, disorder and/or condition
XX caused by expression of a gene controlled by nuclear factor-kappa B (NF-
XX kappaB) or ets. The invention is useful for treating and preventing
XX disorders and conditions caused by expression of a gene controlled by NF-
XX kappaB or ets such as cerebral aneurysm, cancer, Marfan's syndrome,
XX aortic detachment, post-angioplasty restenosis, chronic articular
XX rheumatism, asthma, atopic dermatitis, nephritis, renal failure, and
XX plaque rupture, disorders caused by eosinophilic abnormality such as
XX asthma which includes bronchial asthma, childhood asthma, allergic
XX asthma, atopic asthma, steroid-resistant asthma (SRA), non-allergic
XX asthma, intrinsic asthma, extrinsic asthma, allergic diseases, skin diseases
XX cardiac asthma and infectious asthma. The invention is used in the preparation of vaccines. The
XX and mycosis. The invention is used in the preparation of vaccines. The
XX present sequence is a nuclear factor-kappaB (NF-kappaB) decoy
XX oligonucleotide. This sequence is used in the exemplification of the
XX invention.
XX
XX SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 12; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.9;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CCTTGAAGGGATTTCCTCC 20
XX DB 1 CCTTGAAGGGATTTCCTCC 20
XX
RESULT 13
AAQ90101
ID AAQ90101 standard; DNA; 36 BP.
XX
XX AC AAQ90101;
XX
XX DT 11-JAN-1996 (first entry)
XX
XX DE VCAM-1 expression inhibiting oligonucleotide.
XX
XX KW Vascular cell adhesion molecule; VCAM-1; inhibitory oligonucleotide;
XX transcriptional regulatory factor; diagnosis; treatment; restenosis;
XX atherosclerosis; inflammatory disease; ds.
XX
XX OS Synthetic.
XX
XX PN WO9512415-A1.
XX
XX PD 11-MAY-1995.

```

XX 07-NOV-1994; 94WO-US012797.
 XX
 XX
 XX 05-NOV-1993; 93US-00147878.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX (UYEM-) UNIV EMORY.
 XX Medford RM, Bennett CF;
 XX WPI; 1995-193802/25.
 XX
 XX Oligo-nucleotide(s) which modulate vascular cell adhesion molecule
 PT expression by binding a transcription regulatory element - used to
 PT diagnose and treat atherosclerosis, restenosis or inflammatory disease.
 XX
 XX Claim 17; Page 33; 49pp; English.
 XX
 XX AAQ90100-Q90111 bind the vascular cell adhesion molecule (VCAM)-1 gene
 CC transcriptional regulatory factor, therefore inhibiting the expression of
 CC VCAM-1. They can be used in the diagnosis and treatment of restenosis,
 CC atherosclerosis and inflammatory diseases
 XX
 XX Sequence 36 BP; 3 A; 13 C; 9 G; 11 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 20; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTTGAGGGGATTCCTCC 20
 DB 16 CCTTGAGGGGATTCCTCC 35
 RESULT 14
 AAQ90100
 ID AAQ90100 standard; DNA; 47 BP.
 XX
 XX AC AAQ90100;
 XX
 XX 11-JAN-1996 (first entry)
 DT
 XX VCAM-1 expression inhibiting oligonucleotide.
 DE
 XX Vascular cell adhesion molecule; VCAM-1; inhibitory oligonucleotide;
 KW transcriptional regulatory factor; diagnosis; treatment; restenosis;
 KW atherosclerosis; inflammatory disease; ds.
 XX
 XX Synthetic.
 OS
 XX WO9512415-A1.
 FN
 XX 11-MAY-1995.
 PD
 XX 07-NOV-1994; 94WO-US012797.
 PF
 XX 05-NOV-1993; 93US-00147878.
 PR
 XX (ISIS-) ISIS PHARM INC.
 XX (UYEM-) UNIV EMORY.
 PA
 XX Medford RM, Bennett CF;
 XX WPI; 1995-193802/25.
 DR
 XX Oligo-nucleotide(s) which modulate vascular cell adhesion molecule
 PT expression by binding a transcription regulatory element - used to
 PT diagnose and treat atherosclerosis, restenosis or inflammatory disease.
 XX
 XX Claim 17; Page 33; 49pp; English.
 PS
 XX AAQ90100-Q90111 bind the vascular cell adhesion molecule (VCAM)-1 gene
 CC transcriptional regulatory factor, therefore inhibiting the expression of

CC VCAM-1. They can be used in the diagnosis and treatment of restenosis,
 CC atherosclerosis and inflammatory diseases
 XX
 XX Sequence 47 BP; 3 A; 17 C; 12 G; 15 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 20; DB 2; Length 47;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTTGAGGGGATTCCTCC 20
 DB 22 CCTTGAGGGGATTCCTCC 41
 RESULT 15
 ACF79417
 ID ACF79417 standard; DNA; 130 BP.
 XX
 XX AC ACF79417;
 XX
 XX 18-DEC-2003 (first entry)
 DT
 XX VCAM-1 promoter.
 DE
 XX VCAM-1; promoter; oestrogen; receptor; c-rel; osteoporosis; osteopathic;
 KW ds.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH protein_bind 26..35
 FT /*tag= a
 FT /bound_moiety= "Nuclear factor-kappaB"
 FT protein_bind 40..50
 FT /*tag= b
 FT /bound_moiety= "Nuclear factor-kappaB"
 FT
 XX WO2003071281-A2.
 FN
 XX 28-AUG-2003.
 PD
 XX 21-FEB-2003; 2003WO-EP050027.
 PF
 XX 25-FEB-2002; 2002EP-00075789.
 PR
 XX (ALKU) AKZO NOBEL NV.
 PA
 XX Boersma CJC, Van Gool AJ;
 PI
 XX WPI; 2003-748205/70.
 DR
 XX Measuring a direct interaction between an estrogen receptor and c-Rel in
 PT an in vitro system, for selecting a compound to treat osteoporosis, by
 PT providing for a detection parameter proportionally related to the degree
 PT of the interaction.
 XX
 XX Example; Page 32; 38pp; English.
 PS
 XX The present sequence in that of a cloned selection of the promoter region
 CC of the VCAM-1 gene. The promoter contains nuclear factor-kappaB response
 CC elements. The invention provides a method to measure a direct interaction
 CC between an estrogen receptor and a transactivation protein (c-Rel) in an
 CC in vitro system by providing for a detection parameter proportionally
 CC related to the degree of the interaction. A yeast two-hybrid assay for
 CC the measurement is provided. The detection parameter, i.e. the method
 CC used to measure the interaction, includes the use of promoter reporter
 CC constructs that contain NF-kappaB or estrogen receptor responsive
 CC regulatory elements fused to a heterologous reporter gene capable of
 CC signalling the activation of the regulatory element. The method is useful
 CC for selecting a compound for therapeutic efficacy in osteoporosis
 XX
 XX Sequence 130 BP; 23 A; 43 C; 24 G; 40 T; 0 U; 0 Other;
 SQ

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Query Match 100.0%; Score 20; DB 10; Length 130;
 Best Local Similarity 100.0%; Pred. No. 2.5; 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 |||||
 Db 34 CCTTGAGGGATTCCCTCC 53
 |||||

Search completed: December 28, 2004, 10:15:52
 Job time : 404 secs

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OM nucleic - nucleic search, using sw model

Run on: December 28, 2004, 07:31:07 ; Search time 80 Seconds
(without alignments)
177.697 Million cell updates/sec

Title: US-08-945-805-1

Perfect score: 20

Sequence: 1 ccttgaaggatttcctcc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	20	3	US-08-945-805-1
2	20	100.0	20	4	US-09-166-649B-1
3	20	100.0	36	4	US-08-401-192-2
4	20	100.0	46	4	US-08-401-192-1
5	20	100.0	1032	3	US-08-482-073-8
6	18	90.0	19	4	US-08-401-192-4
7	16.8	84.0	32	4	US-09-474-432B-1507
8	16.8	84.0	32	4	US-09-476-387-1506
9	16.8	84.0	47	4	US-08-474-432B-39
10	16.8	84.0	47	4	US-09-474-432B-40
11	16.8	84.0	47	4	US-09-474-432B-41
12	16.8	84.0	47	4	US-09-474-432B-42
13	16.8	84.0	47	4	US-09-474-432B-43
14	16.8	84.0	47	4	US-09-474-432B-44
15	16.8	84.0	47	4	US-09-474-432B-45
16	16.8	84.0	47	4	US-09-474-432B-46
17	16.8	84.0	47	4	US-09-474-432B-47
18	16.8	84.0	47	4	US-09-474-432B-48
19	16.8	84.0	47	4	US-09-474-432B-49
20	16.8	84.0	47	4	US-09-474-432B-50
21	16.8	84.0	47	4	US-09-474-432B-51
22	16.8	84.0	47	4	US-09-474-432B-52
23	16.8	84.0	47	4	US-09-474-432B-53
24	16.8	84.0	47	4	US-09-474-432B-54
25	16.8	84.0	47	4	US-09-474-432B-55
26	16.8	84.0	47	4	US-09-474-432B-56
27	16.8	84.0	47	4	US-09-474-432B-57

c	28	16.8	84.0	47	4	US-09-474-432B-58	Sequence 58, Appl
c	29	16.8	84.0	47	4	US-09-474-432B-59	Sequence 59, Appl
c	30	16.8	84.0	47	4	US-09-474-432B-60	Sequence 60, Appl
c	31	16.8	84.0	47	4	US-09-474-432B-61	Sequence 61, Appl
c	32	16.8	84.0	47	4	US-09-474-432B-62	Sequence 62, Appl
c	33	16.8	84.0	47	4	US-09-474-432B-63	Sequence 63, Appl
c	34	16.8	84.0	47	4	US-09-474-432B-64	Sequence 64, Appl
c	35	16.8	84.0	47	4	US-09-474-432B-65	Sequence 65, Appl
c	36	16.8	84.0	47	4	US-09-474-432B-66	Sequence 66, Appl
c	37	16.8	84.0	47	4	US-09-474-432B-67	Sequence 67, Appl
c	38	16.8	84.0	47	4	US-09-474-432B-68	Sequence 68, Appl
c	39	16.8	84.0	47	4	US-09-474-432B-69	Sequence 69, Appl
c	40	16.8	84.0	47	4	US-09-474-432B-70	Sequence 70, Appl
c	41	16.8	84.0	47	4	US-09-474-432B-71	Sequence 71, Appl
c	42	16.8	84.0	47	4	US-09-474-432B-72	Sequence 72, Appl
c	43	16.8	84.0	47	4	US-09-474-432B-73	Sequence 73, Appl
c	44	16.8	84.0	47	4	US-09-474-432B-74	Sequence 74, Appl
c	45	16.8	84.0	47	4	US-09-474-432B-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1

US-08-945-805-1
; Sequence 1, Application US/08945805A
; Patent No. 6262033
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, RYUICHI
; APPLICANT: OGIMURA, TOSHIO
; APPLICANT: SUGIMOTO, TOSHIKO
; APPLICANT: MAEDA, KAZUHIRO
; APPLICANT: KAWAMURA, IKUO
; APPLICANT: CHIBA, TOSHIYUKI
; TITLE OF INVENTION: REMEDY AND PREVENTIVE FOR DISEASES CAUSED BY NF-KB
; FILE REFERENCE: 1993-0PCT
; CURRENT APPLICATION NUMBER: US/08/945,805A
; CURRENT FILING DATE: 1998-01-06
; EARLIER APPLICATION NUMBER: PCT/JP96/01234
; EARLIER FILING DATE: 1996-05-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-08-945-805-1

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGATTTCCTCC 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CCTTGAAGGATTTCCTCC 20

RESULT 2

US-09-166-649B-1
; Sequence 1, Application US/09166649B
; Patent No. 6753150
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in The City of New York
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David M
; TITLE OF INVENTION: METHODS FOR DETERMINING WHETHER A COMPOUND IS CAPABLE OF INHIBIT
; TITLE OF INVENTION: INTERACTION OF A PEPTIDE WITH RAGE
; FILE REFERENCE: 56613
; CURRENT APPLICATION NUMBER: US/09/166,649B
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 1

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: Primer
; LOCATION: (1)..(20)
; OTHER INFORMATION: Primer Against Human NF-kB
; FEATURE:
; NAME/KEY: Primer
; LOCATION: (1)..(20)
; OTHER INFORMATION: PCR Primer Against Human NF-kB
; US-09-166-649B-1
;
; Query Match 100.0%; Score 20; DB 4; Length 20;
; Best Local Similarity 100.0%; Pred. No. 0.1; 0; Indels 0; Gaps 0;
; Matches 20; Conservative 0; Mismatches 0;
;
QY 1 CCTGAAGGGATTTCCTCC 20
Db 1 CCTGAAGGGATTTCCTCC 20

RESULT 4
US-08-401-192-1
; Sequence 1, Application US/08401192
; Patent No. 6713621
; GENERAL INFORMATION:
; APPLICANT: Bennett and Medford
; TITLE OF INVENTION: Modulation of selected Gene Expression
; Through No. 6713621el Oligonucleotide Interaction
;
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/401,192
; FILING DATE: 09-Mar-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/147,878
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Caldwell
; REGISTRATION NUMBER: 28,937
; REFERENCE/DOCKET NUMBER: ISIS-1021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; ANTI-SENSE: No
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-401-192-1
;
; Query Match 100.0%; Score 20; DB 4; Length 46;
; Best Local Similarity 100.0%; Pred. No. 0.12; 0; Indels 0; Gaps 0;
; Matches 20; Conservative 0; Mismatches 0;
;
QY 1 CCTGAAGGGATTTCCTCC 20
Db 21 CCTGAAGGGATTTCCTCC 40

RESULT 5
US-08-482-073-8
; Sequence 8, Application US/08482073
; Patent No. 6307025
; GENERAL INFORMATION:
; APPLICANT: Hession, Catherine A.
; APPLICANT: Lobb, Roy R.
; APPLICANT: Goelz, Susan E.
; APPLICANT: Osborn, Laurelee
; APPLICANT: Benjamin, Christopher D.
; APPLICANT: Rosa, Margaret D.
; TITLE OF INVENTION: ENDOTHELIAL CELL-LEUKOCYTE ADHESION
;
; Query Match 100.0%; Score 20; DB 4; Length 36;
; Best Local Similarity 100.0%; Pred. No. 0.12; 0; Indels 0; Gaps 0;
; Matches 20; Conservative 0; Mismatches 0;
;
QY 1 CCTGAAGGGATTTCCTCC 20
Db 21 CCTGAAGGGATTTCCTCC 40

RESULT 3
US-08-401-192-2
; Sequence 2, Application US/08401192
; Patent No. 6713621
; GENERAL INFORMATION:
; APPLICANT: Bennett and Medford
; TITLE OF INVENTION: Modulation of selected Gene Expression
; Through No. 6713621el Oligonucleotide Interaction
;
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/401,192
; FILING DATE: 09-Mar-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/147,878
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Caldwell
; REGISTRATION NUMBER: 28,937
; REFERENCE/DOCKET NUMBER: ISIS-1021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; ANTI-SENSE: No
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-401-192-2
;
; Query Match 100.0%; Score 20; DB 4; Length 36;
; Best Local Similarity 100.0%; Pred. No. 0.12; 0; Indels 0; Gaps 0;
; Matches 20; Conservative 0; Mismatches 0;
;
QY 1 CCTGAAGGGATTTCCTCC 20
Db 1 CCTGAAGGGATTTCCTCC 20

```

;; TITLE OF INVENTION: MOLECULES (BLAMs) AND MOLECULES INVOLVED IN LEUKOCYTE
;; TITLE OF INVENTION: ADHESION (MILAs)
;; NUMBER OF SEQUENCES: 25
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Neave
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: United States of America
;; ZIP: 10020
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/482,073
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,336
;; FILING DATE:
;; APPLICATION NUMBER: US 07/608298
;; FILING DATE: 31-OCT-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US 90/02357
;; FILING DATE: 27-APR-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/452675
;; FILING DATE: 18-DEC-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/359516
;; FILING DATE: 01-JUN-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/354151
;; FILING DATE: 28-APR-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Haley Jr., James F.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: B124CIP4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 596-9000
;; TELEFAX: (212) 596-9090
;; TELEX: 14-8367
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1032 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; US-08-482-073-8

Query Match 100.0%; Score 20; DB 3; Length 1032;
Best Local Similarity 100.0%; Pred. No. 0.25; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20
Db 221 CCTTGAAGGGATTTCCTCC 240

RESULT 6
US-08-401-192-4
; Sequence 4, Application US/08401192
; Patent No. 6713621
; GENERAL INFORMATION:
; APPLICANT: Bennett and Medford
; TITLE OF INVENTION: Modulation of selected Gene Expression
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; Mackiewicz & No. 6713621ris

;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: WORDPERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/401,192
;; FILING DATE: 09-Mar-1995
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/147,878
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: John W. Caldwell
;; REGISTRATION NUMBER: 28,937
;; REFERENCE/DOCKET NUMBER: ISIS-1021
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19
;; TYPE: Nucleic Acid
;; STRANDEDNESS: Double
;; TOPOLOGY: Linear
;; ANTI-SENSE: NO
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-401-192-4

Query Match 90.0%; Score 18; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTGAAGGGATTTCCTCC 20
Db 1 TTGAAGGGATTTCCTCC 18

RESULT 7
US-09-474-432B-1507/c
; Sequence 1507, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1507
; LENGTH: 32
; TYPE: RNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
NAME/KEY: misc feature
LOCATION: (2)..(11)
OTHER INFORMATION: 2'-O-Methyl
NAME/KEY: misc feature
LOCATION: (12)..(16)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (24)..(24)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (27)..(29)
OTHER INFORMATION: 2'-deoxy-2'-amino
US-09-474-432B-1507

Query Match 84.0%; Score 16.8; DB 4; Length 32;
Best Local Similarity 90.0%; Pred. No. 6;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
DB 20 CCTTGAAGGGAGTTTCCTCC 1

RESULT 8
US-09-476-387-1506/c
Sequence 1506, Application US/09476387
Patent No. 6617438
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenka Matulic
APPLICANT: Sweedler, Dave
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
FILE REFERENCE: MBH00-831-C (249/073)
CURRENT APPLICATION NUMBER: US/09/476,387
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 09/474,432
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/301,511
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: 60/083,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/064,866
PRIOR FILING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1506
LENGTH: 32
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
NAME/KEY: misc feature
LOCATION: (2)..(11)
OTHER INFORMATION: 2'-O-Methyl
NAME/KEY: misc feature
LOCATION: (12)..(16)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (24)..(24)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (27)..(29)
OTHER INFORMATION: 2'-deoxy-2'-amino
US-09-476-387-1506

Query Match 84.0%; Score 16.8; DB 4; Length 32;
Best Local Similarity 90.0%; Pred. No. 6;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
DB 20 CCTTGAAGGGAGTTTCCTCC 1

RESULT 9
US-09-474-432B-39/c
Sequence 39, Application US/09474432B
Patent No. 6528640
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Burgin, Alex
APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, David
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
FILE REFERENCE: MBH00-831-B (247/276)
CURRENT APPLICATION NUMBER: US/09/474,432B
CURRENT FILING DATE: 1999-12-19
PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/084,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: US 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 09/301,511
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SOFTWARE: PatentIn version 3.0
SEQ ID NO 39
LENGTH: 47
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
NAME/KEY: misc feature
LOCATION: (1)..(10)
OTHER INFORMATION: 2'-O-Methyl
NAME/KEY: misc feature
LOCATION: (12)..(21)
OTHER INFORMATION: 2'-O-Methyl
NAME/KEY: misc feature
LOCATION: (43)..(47)
OTHER INFORMATION: 2'-O-Methyl
NAME/KEY: misc feature
LOCATION: (22)..(26)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (32)..(32)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (34)..(35)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (37)..(39)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (47)..(47)
OTHER INFORMATION: 3'-end phosphate attached to an inverted deoxybasic moiety, in
US-09-474-432B-39

Query Match 84.0%; Score 16.8; DB 4; Length 47;
Best Local Similarity 90.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20
|||||
Db 30 CCTTGAAGGGATTTCCTCC 11

RESULT 10
US-09-474-432B-40/c
; Sequence 40, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Svedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 47
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (12)..(21)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (43)..(47)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (22)..(26)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc feature
; LOCATION: (34)..(35)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc feature
; LOCATION: (37)..(39)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: 3'-end phosphate attached to an inverted deoxybasic moiety, in a
US-09-474-432B-40

Query Match 84.0%; Score 16.8; DB 4; Length 47;
Best Local Similarity 90.0%; Pred. No. 6.6; 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;
Qy 1 CCTTGAAGGGATTTCCTCC 20
|||||
Db 30 CCTTGAAGGGATTTCCTCC 11

RESULT 11
US-09-474-432B-41/c
; Sequence 41, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Svedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 47
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (12)..(21)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (43)..(47)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (22)..(26)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc feature
; LOCATION: (34)..(35)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc feature
; LOCATION: (37)..(39)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: 3'-end phosphate attached to an inverted deoxybasic moiety, in a
US-09-474-432B-41

Query Match 84.0%; Score 16.8; DB 4; Length 47;
Best Local Similarity 90.0%; Pred. No. 6.6; 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;
Qy 1 CCTTGAAGGGATTTCCTCC 20
|||||
Db 30 CCTTGAAGGGATTTCCTCC 11

RESULT 12
US-09-474-432B-42/c
; Sequence 42, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:

us-08-945-805-1.rn1

Wed Dec 29 09:34:03 2004

```

; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MEH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 47
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (12)..(21)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (43)..(47)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (22)..(26)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (37)..(39)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: 3'-end phosphate attached to an inverted deoxybasic moiety, in
US-09-474-432B-43

Query Match      84.0%; Score 16.8; DB 4; Length 47;
Best Local Similarity 90.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTGAGGGAGTTTCCTCC 20
    |||||
Db 30 CTTGAGGGAGTTTCCTCC 11

RESULT 14
US-09-474-432B-44/c
; Sequence 44, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MEH00-831-B (247/276)

```

```

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MEH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 47
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (12)..(21)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (43)..(47)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (22)..(26)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (37)..(39)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: 3'-end phosphate attached to an inverted deoxybasic moiety, in a
US-09-474-432B-42

Query Match      84.0%; Score 16.8; DB 4; Length 47;
Best Local Similarity 90.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTGAGGGAGTTTCCTCC 20
    |||||
Db 30 CTTGAGGGAGTTTCCTCC 11

RESULT 13
US-09-474-432B-43/c
; Sequence 43, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex

```

; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 47
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
; NAME/KEY: misc_feature
; LOCATION: (12)..(21)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (43)..(47)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (22)..(26)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (34)..(35)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (37)..(39)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: 3'-end phosphate attached to an inverted deoxyabasic moiety, in a

US-09-474-432B-44

Query Match 84.0%; Score 16.8; DB 4; Length 47;
Best Local Similarity 90.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20
||| ||||| ||| |||||
Db 30 CCTTGAAGGGAGTTTCCTCC 11

RESULT 15

US-09-474-432B-45/c
; Sequence 45, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MEHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727

; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 47
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (12)..(21)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (43)..(47)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (22)..(26)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (34)..(35)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (37)..(39)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: 3'-end phosphate attached to an inverted deoxyabasic moiety, in a

US-09-474-432B-45

Query Match 84.0%; Score 16.8; DB 4; Length 47;
Best Local Similarity 90.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20
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Db 30 CCTTGAAGGGAGTTTCCTCC 11

Search completed: December 28, 2004, 09:18:57
Job time : 81 secs

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OM nucleic - nucleic search, using sw model

Run on: December 28, 2004, 10:09:11 ; Search time 3939 Seconds
(without alignments)
28.272 Million cell updates/sec

Title: US-08-945-805-1

Perfect score: 20

Sequence: 1 ccttgaaggattccctcc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4105333 seqs, 2784095677 residues

Total number of hits satisfying chosen parameters: 8210666

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	20	100.0	20	9	US-09-832-841-1
2	20	100.0	20	10	US-09-937-839-1
3	20	100.0	20	10	US-09-166-649B-1
4	20	100.0	20	16	US-10-466-239-1
5	20	100.0	20	17	US-10-618-362A-1
6	20	100.0	20	17	US-10-618-362A-14
7	20	100.0	20	17	US-10-783-635-1
8	20	100.0	20	17	US-10-366-718-1
9	20	100.0	20	17	US-10-468-717-1
10	20	100.0	20	18	US-10-824-757-1
11	20	100.0	1032	15	US-10-234-041-9
12	18	90.0	554	16	US-10-424-599-51726

C 13	17	85.0	708	16	US-10-343-650A-97	Sequence 97, Appl
C 14	16.8	84.0	32	10	US-09-825-805-1548	Sequence 1548, Ap
C 15	16.8	84.0	40	10	US-09-916-466-399	Sequence 399, App
C 16	16.8	84.0	40	10	US-09-916-466-400	Sequence 400, App
C 17	16.8	84.0	40	10	US-09-916-466-401	Sequence 401, App
C 18	16.8	84.0	40	10	US-09-916-466-402	Sequence 402, App
C 19	16.8	84.0	40	10	US-09-916-466-403	Sequence 403, App
C 20	16.8	84.0	40	10	US-09-916-466-404	Sequence 404, App
C 21	16.8	84.0	40	10	US-09-916-466-405	Sequence 405, App
C 22	16.8	84.0	40	10	US-09-916-466-406	Sequence 406, App
C 23	16.8	84.0	40	10	US-09-916-466-407	Sequence 407, App
C 24	16.8	84.0	40	10	US-09-916-466-408	Sequence 408, App
C 25	16.8	84.0	40	10	US-09-916-466-409	Sequence 409, App
C 26	16.8	84.0	40	10	US-09-916-466-410	Sequence 410, App
C 27	16.8	84.0	40	10	US-09-916-466-411	Sequence 411, App
C 28	16.8	84.0	40	10	US-09-916-466-412	Sequence 412, App
C 29	16.8	84.0	40	10	US-09-916-466-413	Sequence 413, App
C 30	16.8	84.0	40	10	US-09-916-466-414	Sequence 414, App
C 31	16.8	84.0	40	10	US-09-916-466-415	Sequence 415, App
C 32	16.8	84.0	40	10	US-09-916-466-416	Sequence 416, App
C 33	16.8	84.0	40	10	US-09-916-466-417	Sequence 417, App
C 34	16.8	84.0	40	10	US-09-916-466-418	Sequence 418, App
C 35	16.8	84.0	40	10	US-09-916-466-419	Sequence 419, App
C 36	16.8	84.0	40	10	US-09-916-466-420	Sequence 420, App
C 37	16.8	84.0	40	10	US-09-916-466-421	Sequence 421, App
C 38	16.8	84.0	40	10	US-09-916-466-422	Sequence 422, App
C 39	16.8	84.0	40	10	US-09-916-466-423	Sequence 423, App
C 40	16.8	84.0	40	10	US-09-916-466-424	Sequence 424, App
C 41	16.8	84.0	40	10	US-09-916-466-425	Sequence 425, App
C 42	16.8	84.0	40	10	US-09-916-466-426	Sequence 426, App
C 43	16.8	84.0	40	10	US-09-916-466-427	Sequence 427, App
C 44	16.8	84.0	40	10	US-09-916-466-428	Sequence 428, App
C 45	16.8	84.0	40	10	US-09-916-466-429	Sequence 429, App

ALIGNMENTS

RESULT 1
US-09-832-841-1
; Sequence 1, Application US/09832841
; Patent No. US20020098162A1
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, RYUICHI
; APPLICANT: OGIMURA, TOSHIO
; APPLICANT: SUGIMOTO, TOSHIKO
; APPLICANT: MAEDA, KAZUHIRO
; APPLICANT: KAWAMURA, IKUO
; APPLICANT: CHIBA, TOSHIYUKI
; TITLE OF INVENTION: REMEDY AND PREVENTIVE FOR DISEASES CAUSED BY NF-KB
; FILE REFERENCE: 18993-OPCT
; CURRENT APPLICATION NUMBER: US/09/832,841
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 08/945,805
; PRIOR FILING DATE: 1998-01-06
; PRIOR APPLICATION NUMBER: PCT/JP96/01234
; PRIOR FILING DATE: 1996-05-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
US-09-832-841-1

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGATTCCCTCC 20
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Wed Dec 29 09:34:04 2004

us-08-945-805-1.1.rnpb

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Db      1  CCTTGAAGGGATTTCCTCC 20

RESULT 2
US-09-937-839-1
; Sequence 1, Application US/09937839
; Publication No. US20030013195A1
; GENERAL INFORMATION:
; APPLICANT: Kaneda, Yasufumi
; TITLE OF INVENTION: Virus Envelope Vector for Gene Transfer
; FILE REFERENCE: 59150-8010
; CURRENT APPLICATION NUMBER: US/09/937.839
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: PCT/JP01/00782
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: JP 2000-25596
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-937-839-1

Query Match      100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CCTTGAAGGGATTTCCTCC 20
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Db      1  CCTTGAAGGGATTTCCTCC 20

RESULT 3
US-09-166-649B-1
; Sequence 1, Application US/09166649B
; Publication No. US20030087302A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in The City of New York
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David M
; TITLE OF INVENTION: METHODS FOR DETERMINING WHETHER A COMPOUND IS CAPABLE OF INHIBITING
; FILE REFERENCE: 56613
; CURRENT APPLICATION NUMBER: US/09/166.649B
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: Primer
; LOCATION: (1)..(20)
; OTHER INFORMATION: Primer Against Human NF-KB
; FEATURE:
; NAME/KEY: Primer
; LOCATION: (1)..(20)
; OTHER INFORMATION: PCR Primer Against Human NF-KB
US-09-166-649B-1

Query Match      100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CCTTGAAGGGATTTCCTCC 20
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Db      1  CCTTGAAGGGATTTCCTCC 20

RESULT 4
US-10-466-239-1
; Sequence 1, Application US/10466239
; Publication No. US20040072726A1
; GENERAL INFORMATION:
; APPLICANT: Ryuchi Morishita
; APPLICANT: Motokuni Aoki
; APPLICANT: Toshio Ogiwara
; APPLICANT: Tomio Kawasaki
; FILE REFERENCE: ANGES-1 US
; CURRENT APPLICATION NUMBER: US/10/466,239
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: PCT/JP02/00865
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NF-?B decoy
; PUBLICATION INFORMATION:
US-10-466-239-1

Query Match      100.0%; Score 20; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CCTTGAAGGGATTTCCTCC 20
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Db      1  CCTTGAAGGGATTTCCTCC 20

RESULT 5
US-10-618-362A-1
; Sequence 1, Application US/10618362A
; Publication No. US20040109843A1
; GENERAL INFORMATION:
; APPLICANT: Ryuchi Morishita
; APPLICANT: Motokuni Aoki
; APPLICANT: Toshio Ogiwara
; APPLICANT: Tomio Kawasaki
; APPLICANT: Hirofumi Makino
; TITLE OF INVENTION: Pharmaceutical composition containing decoy and use of the same
; FILE REFERENCE: ANGES-1 CIP US
; CURRENT APPLICATION NUMBER: US/10/618,362A
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: PCT/JP02/00865
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NF-kappaB Decoy
US-10-618-362A-1

Query Match      100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CCTTGAAGGGATTTCCTCC 20
      |||
Db      1  CCTTGAAGGGATTTCCTCC 20

RESULT 6
US-10-618-362A-14/c

Query Match      100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CCTTGAAGGGATTTCCTCC 20
      |||
Db      1  CCTTGAAGGGATTTCCTCC 20
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; Sequence 14, Application US/10618362A
; Publication No. US20040109843A1
; GENERAL INFORMATION:
; APPLICANT: Ryuichi Morishita
; APPLICANT: Motokuni Aoki
; APPLICANT: Toshio Ogiwara
; APPLICANT: Tomio Kawasaki
; APPLICANT: Hirofumi Makino
; TITLE OF INVENTION: Pharmaceutical composition containing decoy and use of the same
; FILE REFERENCE: ANGES-1 CIP US
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: PCT/JP02/00865
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NF-kappaB Decoy
US-10-618-362A-14

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20
Db 20 CCTTGAAGGGATTTCCTCC 1

RESULT 7
US-10-783-635-1
; Sequence 1, Application US/10783635
; Publication No. US2004014239A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in The City of New York
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David M
; TITLE OF INVENTION: METHODS FOR DETERMINING WHETHER A COMPOUND IS CAPABLE OF INHIBITING
; FILE REFERENCE: 56613
; CURRENT APPLICATION NUMBER: US/10/783.635
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US/09/166,649
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: Primer
; LOCATION: (1)..(20)
; OTHER INFORMATION: Primer Against Human NF-kB
; NAME/KEY: Primer
; LOCATION: (1)..(20)
; OTHER INFORMATION: PCR Primer Against Human NF-kB
US-10-783-635-1

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20
Db 1 CCTTGAAGGGATTTCCTCC 20

RESULT 8
US-10-366-718-1
; Sequence 1, Application US/10366718
; Publication No. US20040162250A1
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, RYUICHI
; APPLICANT: OGIWARA, TOSHIO
; APPLICANT: SUGIMOTO, TOSHIKO
; APPLICANT: MAEDA, KAZUHIRO
; APPLICANT: KAWAMURA, IKUO
; APPLICANT: CHIBA, TOSHIYUKI
; TITLE OF INVENTION: REMEDY AND PREVENTIVE FOR DISEASES CAUSED BY NF-KB
; FILE REFERENCE: 18993-OPCT
; CURRENT APPLICATION NUMBER: US/10/366,718
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US/09/832,841
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 08/945,805
; PRIOR FILING DATE: 1998-01-06
; PRIOR APPLICATION NUMBER: PCT/JP96/01234
; PRIOR FILING DATE: 1996-05-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-366-718-1

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20
Db 1 CCTTGAAGGGATTTCCTCC 20

RESULT 9
US-10-468-717-1
; Sequence 1, Application US/10468717
; Publication No. US20040162251A1
; GENERAL INFORMATION:
; APPLICANT: Ryuichi Morishita
; APPLICANT: Motokuni Aoki
; APPLICANT: Toshio Ogiwara
; APPLICANT: Yasufumi Kaneda
; APPLICANT: Hiroshige Nakamura
; TITLE OF INVENTION: Pharmaceutical composition containing decoy and method of using t
; FILE REFERENCE: ANGES-2 US
; CURRENT APPLICATION NUMBER: US/10/468,717
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: PCT/JP02/00990
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 2001-44350
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NF-kappaB Decoy
US-10-468-717-1

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-08-945-805-1.rnpb

Wed Dec 29 09:34:04 2004

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QY 1 CCTTGAAGGGATTTCCTCC 20
Db 1 CCTTGAAGGGATTTCCTCC 20

LENGTH: 1032
TYPE: DNA
ORGANISM: Homo Sapien
US-10-234-041-9

Query Match
Best Local Similarity 100.0%; Score 20; DB 15; Length 1032;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
Db 221 CCTTGAAGGGATTTCCTCC 240

RESULT 12
US-10-424-599-51726
Sequence 51726, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 51726
LENGTH: 554
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_17722C.1
US-10-424-599-51726

Query Match
Best Local Similarity 90.0%; Score 18; DB 16; Length 554;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 18
Db 421 CCTTGAAGGGATTTCCTCC 438

RESULT 13
US-10-343-650A-97/c
Sequence 97, Application US/10343650A
Publication No. US20040067499A1
GENERAL INFORMATION:
APPLICANT: HAGA, TATSUYA
TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
FILE REFERENCE: 31671-186347
CURRENT APPLICATION NUMBER: US/10/343,650A
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: JP 2000/237818
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: JP 2001/34434
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 694
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 97
LENGTH: 708
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(708)
US-10-343-650A-97

Query Match
Best Local Similarity 85.0%; Score 17; DB 16; Length 708;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
Db 1 CCTTGAAGGGATTTCCTCC 20

LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic oligonucleotide
US-10-824-757-1

Query Match
Best Local Similarity 100.0%; Score 20; DB 18; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
Db 1 CCTTGAAGGGATTTCCTCC 20

RESULT 11
US-10-234-041-9
Sequence 9, Application US/10234041
Publication No. US20030153731A1
GENERAL INFORMATION:
APPLICANT: Biogen, Inc.
APPLICANT: Hession, Catherine A.
APPLICANT: Lobb, Roy R.
APPLICANT: Goelz, Susan E.
APPLICANT: Osborn, Laurelee
APPLICANT: Benjamin, Christopher D.
APPLICANT: Rosa, Margaret D.
TITLE OF INVENTION: Endothelial Cell-Leukocyte Adhesion
FILE REFERENCE: 124CP2DV2CN
CURRENT APPLICATION NUMBER: US/10/234,041
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: 08/473,764
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/342,642
PRIOR FILING DATE: 1994-11-21
PRIOR APPLICATION NUMBER: 07/608,298
PRIOR FILING DATE: 1990-10-31
PRIOR APPLICATION NUMBER: 07/452,675
PRIOR FILING DATE: 1989-12-18
PRIOR APPLICATION NUMBER: 07/359,516
PRIOR FILING DATE: 1989-06-01
PRIOR APPLICATION NUMBER: 07/345,151
PRIOR FILING DATE: 1989-04-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTTGAAGGGATTTCCTCC 17
Db 562 CCTTGAAGGGATTTCCTCC 546

RESULT 14
US-09-825-805-1548/c
; Sequence 1548, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Belgelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides
; FILE REFERENCE: MBHB00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825.805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1548
; LENGTH: 32
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (2)..(11)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (12)..(16)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (24)..(24)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (27)..(29)
; OTHER INFORMATION: 2'-deoxy-2'-amino
US-09-825-805-1548

Query Match 84.0%; Score 16.8; DB 10; Length 32;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCTTGAAGGGATTTCCTCC 20
Db 20 CCTTGAAGGGATTTCCTCC 1

RESULT 15
US-09-916-466-399/c
; Sequence 399, Application US/09916466
; Publication No. US20030064945A1
; GENERAL INFORMATION:
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; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Akhtar, Saghir
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-J (400/032)
; CURRENT APPLICATION NUMBER: US/09/916.466
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 399
; LENGTH: 40
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molecules
US-09-916-466-399

Query Match 84.0%; Score 16.8; DB 10; Length 40;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCTTGAAGGGATTTCCTCC 20
Db 24 CCTTGAAGGGATTTCCTCC 5

Search completed: December 28, 2004, 13:15:13
Job time : 3940 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 28, 2004, 07:31:07 ; Search time 2988 Seconds
(without alignments)
243.907 Million cell updates/sec

Title: US-08-945-805-1

Perfect score: 20

Sequence: 1 ccttgaaggattccctcc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_hic.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_gse1.*
- 9: gb_gse2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	334	5	BY150286
2	20	100.0	701	2	BF385710
3	20	100.0	768	9	CR139070
4	18	90.0	504	7	CO695591
5	18	90.0	604	8	CG133636
6	18	90.0	627	5	BW242276
7	17.4	87.0	269	2	BB002216
8	17.4	87.0	453	6	CA857737
9	17.4	87.0	478	4	BX072801
10	17.4	87.0	529	5	BX844476
11	17.4	87.0	580	4	BM179747
12	17.4	87.0	606	7	CR585617
13	17.4	87.0	671	5	BX850643
14	17.4	87.0	885	6	CC0303290
15	17.4	87.0	938	8	CC091597
16	17.4	87.0	1146	4	BG531353
17	17.4	87.0	1172	8	CC232703
18	17.4	87.0	1172	8	CC302265
19	17	85.0	350	7	R25866
20	17	85.0	512	2	BB755468
21	17	85.0	831	4	BI870073
22	16.8	84.0	152	2	BB064146
23	16.8	84.0	202	9	CG632344
24	16.8	84.0	246	2	AW571808

c	25	16.8	84.0	258	2	AW190931
c	26	16.8	84.0	265	1	AI367826
c	27	16.8	84.0	294	5	BQ102591
c	28	16.8	84.0	306	8	AZ480348
c	29	16.8	84.0	371	1	AA775085
c	30	16.8	84.0	376	1	AA055416
c	31	16.8	84.0	377	5	BY583522
c	32	16.8	84.0	397	8	CC178434
c	33	16.8	84.0	405	2	BF038388
c	34	16.8	84.0	413	8	AZ429984
c	35	16.8	84.0	426	7	H02051
c	36	16.8	84.0	430	5	BY482479
c	37	16.8	84.0	436	7	T93077
c	38	16.8	84.0	446	7	CO298103
c	39	16.8	84.0	455	9	CE433772
c	40	16.8	84.0	466	1	AA054954
c	41	16.8	84.0	468	6	BY661708
c	42	16.8	84.0	478	8	BH098047
c	43	16.8	84.0	491	6	CF166444
c	44	16.8	84.0	496	1	AA624941
c	45	16.8	84.0	504	6	CA654764

ALIGNMENTS

RESULT 1
BY150286
LOCUS
DEFINITION
BY150286 RIKEN full-length enriched, 334 bp mRNA linear EST 10-DEC-2002
Mus musculus cDNA clone U930275P17 5', mRNA sequence.

ACCESSION
BY150286
VERSION
BY150286.1
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
1 (bases 1 to 334)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, O., Saito, R., Saito, H., Yamana, H., Hasegawa, Y., Nogami, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Hill, D.P., Bult, C., Schonbach, C., Gojobori, T., Baldarelli, R., Kanapin, A., Matsuda, H., Hume, D.A., Quackenbush, J., Schriml, L.M., Bradt, D., Brusio, V., Batalov, S., Beisel, K.W., Blake, J.A., Bratt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalia, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongsaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sander, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Varadar, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ichii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sakaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

ANALYSIS
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken.
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES
source
Location/Qualifiers
1..334
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="L930275P17"
/tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
whole body"

ORIGIN
Query Match 100.0%; Score 20; DB 5; Length 334;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTCCCTCC 20
DB 199 CCTTGAAGGGATTCCCTCC 218
BF385710 701 bp mRNA linear EST 27-NOV-2000
602047366F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:4196681 5',
mRNA sequence.

ACCESSION BF385710
VERSION BF385710.1 GI:11367015
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 701)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM9534 row: c column: 18
High quality sequence stop: 699.

FEATURES

source
Location/Qualifiers
1..701
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4196681"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP L19"
/note="Organ: Liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 701;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTCCCTCC 20
DB 162 CCTTGAAGGGATTCCCTCC 181

RESULT 3

CR139070 768 bp DNA linear GSS 06-JUL-2004
LOCUS Reverse strand read from insert in 3'HPRT insertion targeting and
DEFINITION chromosome engineering clone MHPP137g11, genomic survey sequence.
ACCESSION CR139070
VERSION CR139070.1 GI:49886797
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 768)
ADAMS, D.J., BIGGS, P.J., COX, A.V., DAVIES, R.M., VAN DER WEYDEN, L.,
JONKERS, J., SMITH, J., PLUMB, R.W., TAYLOR, R.G., NISHIJIMA, I., YU, Y.,
ROGERS, J. and BRADLEY, A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. <http://www.sanger.ac.uk/MICER>
Location/Qualifiers
1..768
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPP137g11"
/clone_lib="MHPP"

FEATURES

source

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 768;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTCCCTCC 20
DB 636 CCTTGAAGGGATTCCCTCC 655

RESULT 4

CO695591
LOCUS
DEFINITION
ACCESSION
VERSION

FEATURES

source

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 768;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES

source

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KEYWORDS
SOURCE  EST.
ORGANISM  Canis familiaris (dog)
          Canis familiaris
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS  1 (bases 1 to 504)
          Schluter, T., Hermans, J., Weindel, M., Schuette, D., Kranz, H.,
          Henrich, J., and Loebbert, R.
TITLE    Dog arrayTAG cDNA clone collection
JOURNAL  Unpublished (2004)
COMMENT  Contact: Thomas Schluter
          LION bioscience AG
          Waldhoferstrasse 98, D-69123 Heidelberg, Germany
          Tel: +49 6221 4038 150
          Fax: +49 6221 4038 290
          Email: Thomas.Schluter@lionbioscience.com.

FEATURES
Source
Location/Qualifiers
1..504
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="kidney"
/dev_stage="adult"
/lab_hosts="DH10B"
/clone_lib="DGII-kidney"
/note="Organ: kidney; Vector: Dog pBluescript LION"

ORIGIN
Query Match      90.0%; Score 18; DB 7; Length 504;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3 TTGAAGGATTTCCTCC 20
    |||||
Db  440 TTGAAGGATTTCCTCC 457

RESULT 5
CC133636/c
LOCUS      604 bp DNA linear GSS 16-APR-2003
DEFINITION NDL.80H15.T7 Notre Dame Liverpool Aedes aegypti genomic clone
            NDL.80H15, genomic survey sequence.
ACCESSION  CC133636
VERSION     CC133636.1 GI:30002691
KEYWORDS    GSS.
SOURCE      Aedes aegypti (yellow fever mosquito)
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes;
            Stegomyia.
REFERENCE   1 (bases 1 to 604)
AUTHORS    Loftus, B., Shetty, J., Knudson, D. and Severson, D.
TITLE      BAC end sequencing of Aedes aegypti
JOURNAL    Unpublished (2003)
COMMENT    Other GSSs: NDL.80H15.SP6
            Contact: Brendan Loftus
            Department of Eukaryotic Genomics
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-3543
            Fax: 301-838-0208
            Email: enta@tigr.org
            Library was provided by David Severson
            Seq primer: T7
            Class: BAC ends.

FEATURES
Source
Location/Qualifiers
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/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
/clone="NDL.80H15"

/clone_lib="Notre Dame Liverpool"
/note="vector: pECBAC1; Site 1: Hind III; The library was
prepared from whole body tissue of newly hatched L1 larvae
by David Severson at the University of Notre Dame and
Hongbin Zhang"

ORIGIN
Query Match      90.0%; Score 18; DB 8; Length 604;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CCTTGAGGGATTTCCTC 18
    |||||
Db  159 CCTTGAGGGATTTCCTC 142

RESULT 6
BW242276/c
LOCUS      627 bp mRNA linear EST 09-NOV-2002
DEFINITION BW242276 Nori Satoh unpublished cDNA library, tailbud embryo Ciona
            intestinalis cDNA clone citb10ln15 5', mRNA sequence.
ACCESSION  BW242276
VERSION     BW242276.1 GI:24822194
KEYWORDS    EST.
SOURCE      Ciona intestinalis
ORGANISM    Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1 (bases 1 to 627)
AUTHORS    Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
TITLE      Expressed genes in Ciona intestinalis (2002c)
JOURNAL    Unpublished (2002)
COMMENT    Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
Source
Location/Qualifiers
1..627
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="citb10ln15"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud
embryo"

ORIGIN
Query Match      90.0%; Score 18; DB 5; Length 627;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 CTTGAAGGGATTTCCTC 19
    |||||
Db  451 CTTGAAGGGATTTCCTC 434

RESULT 7
BB002216
LOCUS      269 bp mRNA linear EST 22-JUN-2000
DEFINITION BB002216 RIKEN full-length enriched, 0 day neonate skin Mus
            musculus cDNA clone 4631430K12 3', similar to D80005 Human mRNA for
            KIAA0183 gene, mRNA sequence.
ACCESSION  BB002216
VERSION     BB002216.1 GI:8091661
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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	Matches	18;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	2	CTTCAAGGGATTTCCTCC	20							
	123	CTTCAAGGGATTTCCTCC	141							

RESULT	8
CA8577737	
LOCUS	
DEFINITION	
CA8577737	linear mRNA
i196b12.x1	453 bp
Kaestner pgn3 - Mus musculus cDNA clone IMAGE: 3,	
Accession: U09355	
Source: mouse	
Protein:	
MDL:	
FASTA:	
TrEMBL:	
SwissProt:	
RefSeq:	
GeneID:	
Ensembl:	
UniProt:	
NCBI:	
EST	EST 17-DEC-2002

CA857737
ACCESSION
CA857737.1 GI:27161220
VERSION
KEYWORDS
CORNER
Mus musculus (house mouse)
EST.

ORGANISM

Mus musculus

Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa;
Mammalia; Eutheria;
(bases 1 to 453)

Chordata; Vertebrata; Euteleostomi;
Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1. (bases 1 to 453)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blustain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsegarsishvili, R., Williams, T., Jackson, Y., and Bowers, Y.

TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)

CONTACT: Douglas Melton, Klaus H. Kaesner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biochp.harvard.edu
 Pancreas was obtained from Gerard Gradwohl (PNAS 97 E1607-1611,
 2000) Library was constructed by Catherine Lee DNA sequencing by:
 Washington University Genome Sequencing Center for information on
 obtaining a clone please contact: Dr. Marie Scarsee
 (marsee@mail.med.upenn.edu)
 Seq primer: -40UP from Gibco
 up, quality sequence stop: 196.

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FEATURES             Location/Qualifiers
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         /mol_type="mRNA"
         /strain="129/Sv x CD1"
         /db_xref="taxon:10090"
         /clone="IMAGE:"
         /dev_stage="p.c. 14.5"
         /lab_host="E. coli-DH12S (GIBCO)"
         /clone_lib="Kaestner ngn3 -"
         /note="Organ: pancreas; Vector: pSPORT2 (GIBCO); Site:1:
Not 1; Site 2: Sal I; The library was prepared by
Catherine S_ Lee and has not been published. The pancreas
was obtained from Gerard Gradwohl (PNAS 97 p1607-1611,
2000). The cDNA's were prepared with an oligo containing a
NotI site, and SalI linkers were added to the ends. The
NotI-SalI sites in the vectors. This is one of two
libraries, ngn3 wt and ngn3 -/- . The ngn3 -/- library is
in pSPORT2. T7 promoter is 3'."

```

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ORIGIN
      87.0%;   Score 17.4; DB 6;   Length 453;
Query Match    94.7%;   Pred.No. 7.8e+0;
Best Local Similarity
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCTTGAAGGGATTTCCTC 19
          |||||
nb      83 CCTTGAAGGGATTTCAC 101
```

1. (bases 1 to 269)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Iizawa, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., M., Oda, H.,
Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,
Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,
Shibata, K., Shibata, Y., Shigenoto, Y., Shingawa, A., Shiraki, T.,
Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,
Takahashi, F., Tomimaga, N., Toyota, T., Tsunoda, Y., Watahiki, A.,
Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A.,
Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and
Hasegahizaki, Y.

TITLE	COMMENT
RIKEN Mouse ESTs (Konno.H., et al.) Unpublished (2000)	Contact: Yoshihide Hayaishizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222

Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: <http://genome.sgc.riken.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoaka, S.,
Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998)
Itoh, M., Kitsuina, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. *Genome Res.* 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

FEATURES	source
Location/Qualifiers	
1. 269	
/organism="Mus musculus"	
/mol_type="mRNA"	
/strain="CS7BL/6J"	
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/clone="4631430K12"	
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/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCACAGAGCTCTTTTCTTTTCTTNN 3'], cDNA was prepared by using trehalase thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGATTAAATTAATATCCCTCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"	

ORIGIN	Score	DB 2;	Length
Query Match	87.0%	17.4;	269;
Best Local Similarity	94.7%	Pred. NO. 7.2e+02;	

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RESULT 9
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LOCUS
DEFINITION
  BJ072801 NIBB Mochii mRNA linear EST 29-SEP-2003
  laevis cDNA clone XL099p17 5', mRNA sequence.
ACCESSION
  BJ072801
VERSION
  BJ072801.1 GI:17502990
KEYWORDS
  EST.
SOURCE
  Xenopus laevis (African clawed frog)
ORGANISM
  Xenopus laevis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
  Xenopodinae; Xenopus.
REFERENCE
  1 (bases 1 to 478)
  Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
  Kohara,Y.
  Expressed genes in X. laevis embryo
  Unpublished (2001)
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp
  The information of this clone is available through the following
  URL.
  http://xenopus.nibb.ac.jp.
FEATURES
  source
    Location/Qualifiers
      1..478
        /organism="Xenopus laevis"
        /mol_type="mRNA"
        /db_xref="taxon:8355"
        /clone="XL099p17"
        /tissue_type="whole embryo"
        /dev_stage="stage 25"
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        library"
ORIGIN
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  Best Local Similarity 94.7%; Pred. No. 7.9e+02;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  Oy 2 CTTGAAGGGATTTCCTCC 20
      |||||
  Db 336 CTTGAAGGGATTTCCTCC 318

RESULT 10
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LOCUS
DEFINITION
  BX844476 NICHG_XGC_Emb1 Xenopus laevis cDNA clone IMAGE:4959036
  ; IMAGE:6633714 5', mRNA sequence.
ACCESSION
  BX844476
VERSION
  BX844476.1 GI:39734522
KEYWORDS
  EST.
SOURCE
  Xenopus laevis (African clawed frog)
ORGANISM
  Xenopus laevis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
  Xenopodinae; Xenopus.
REFERENCE
  1 (bases 1 to 529)
  Heil,O., Neubert,P., Petera,M., Radelof,U., Schneider,D.,
  Schroth,A., Korn,B. and Landgrebe,J
  Xenopus laevis UniGene Set 1 (RZPDLib No.988)
  Unpublished (2003)
  Contact: Ina Rolfs
  RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
  Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
  RZPD; IMAGE:6633714.205.
  RZPDLib; I.M.A.G.E. cDNA Clone Collection (amp- resistant) (RZPDLib

```

```

No.998) http://www.rzpd.de/cgi-
bin/products/showLib.pl.cgi/response?libNo=998 RZPDLib; Xenopus
laevis UniGene Set 1 (RZPDLib No.988) http://www.rzpd.de/cgi-
bin/products/showLib.pl.cgi/response?libNo=988 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
SP6, 5' ATTAGGTGACACTATAG 3'.
FEATURES
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    Location/Qualifiers
      1..529
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        /clone="IMAGE:6633714"
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        /lab_host="DH10B (phage-resistant)"
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        is a Xenopus Gene Collection (XGC) library."
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  Query Match 87.0%; Score 17.4; DB 5; Length 529;
  Best Local Similarity 94.7%; Pred. No. 8e+02;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  Oy 2 CTTGAAGGGATTTCCTCC 20
      |||||
  Db 182 CTTGAAGGGATTTCCTCC 164

RESULT 11
BM179747/c
LOCUS
DEFINITION
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  5', similar to TR:095197 095197 RETICULON PROTEIN. ;, mRNA sequence.
ACCESSION
  BM179747
VERSION
  BM179747.1 GI:17403818
KEYWORDS
  EST.
SOURCE
  Xenopus laevis (African clawed frog)
ORGANISM
  Xenopus laevis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
  Xenopodinae; Xenopus; Xenopus.
REFERENCE
  1 (bases 1 to 580)
  NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Other_ESTs: da1ld07.xl
  Contact: Robert Strausberg, Ph.D.
  Email: cgaps-r@mail.nih.gov
  Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: Xenopus clones from this library are available
  through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
  Seq primer: -40RP from Gibco
  High quality sequence stop: 442.
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BX850643.1 GI:39739085

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Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Crania
Amphibia; Batrachia; Anura; Mesobatrachodinae; Xenopus; Xenopus.

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Helli, O., Newert, F., Korsch, M.,
Schroth, A., Korn, B. and Landgrebe, J.
Xenopus laevis UniGene Set 1 (RZPDLI-
2002-0001) (2002)

RZPD Deutsches Ressourcenzentrum
Im Neuenheimer Feld 580, D-69120 Heidelberg
RZPD; IMAGp998H1310927.

bin/products/showLib.pl.cgi/responses
laevis UniGene Set 1 (RZPDLIB No.98)
bin/products/showLib.pl.cgi/responses
RZPD Deutsches Ressourcenzentrum fuer
Heubnerweg 6, D-14059 Berlin Germany

Tel: +49 30 32632 111
 Fax: +49 30 32632 111
 www.rzpd.de
 This clone is available royalty-free
 contact RZPD (clone@rzpd.de) for fu
 SP6, 5' ATTAGGTGACACTATAG 3'.
 Location/Qualifiers
 1..671

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 Not1; Site_2: SalI; Cloned
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 Technologies. Note: This i
 (XGC) library."

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ch      87.0%; Score 17.4;
l Similarity 94.7%; Pred. No. 8.4;
18; Conservative 0; Mismatches
2 CTTGAAGGGATTCCCTCC 20
|||||
148 CTTGAAGGGATGTCCTCC 330

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CT303290 885 bp

AGENCOURT 14233231 NICHD_XGC_Brn1
IMAGE:6955529 5', mRNA sequence.
CD303290
CD303290.1 GI:31083109

Xenopus laevis (African Clawed Frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Cran
Amphibia; Batrachia; Anura; Mesoba

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mam
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics

National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement:

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: L1AM14581 Row: c column: 16
High quality sequence stop: 687.

FEATURES

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/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."

ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 885;
Best Local Similarity 94.7%; Pred. No. 8.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTTGAAGGGATTTCCTCC 20
|||||
Db 337 CTTGAAGGGATTTCCTCC 319

RESULT 15

CC091597
LOCUS
DEFINITION
CSU-K33r.24N21.T7 CSU-K33r Aedes aegypti genomic clone
CSU-K33r.24N21, genomic survey sequence.

CC091597
ACCESSION
CC091597.1 GI:29950049

VERSION
KEYWORDS
SOURCE

ORGANISM
Aedes aegypti (yellow fever mosquito)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
Stegomyia.

REFERENCE
1 (bases 1 to 938)

Loftus, B., Shetty, J., Severson, D., Brown, S. and Knudson, D.

End sequencing of Aedes aegypti BACs

Unpublished (2003)

Other GSSs: CSU-K33r.24N21.SP6

Contact: Brendan Loftus

Department of Eukaryotic Genomics

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: enta@tigr.org

Library was provided by Susan Brown and Dennis Knudson at Colorado
State University.

Seq primer: T7

Class: BAC ends.

FEATURES

Location/Qualifiers
1. .938
/organism="Aedes aegypti"
/mol_type="genomic DNA"
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/clone="CSU-K33r.24N21"

/clone_lib="CSU-K33r"
/note="Vector: pBelosAC11; Site_1: HindIII"

ORIGIN

Query Match 87.0%; Score 17.4; DB 8; Length 938;
Best Local Similarity 94.7%; Pred. No. 8.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAAGGGATTTCCTC 19
|||||
Db 846 CTTGAAGGGATTTCCTC 864

Search completed: December 28, 2004, 10:09:04
Job time : 2996 secs

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